

1 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCCTG
 51 CGCCAGGATG GAGTTCTGAA AATGCCCTGG CCACCCCCGAA GAGTTCTACA
 101 ACCTGGTGCAG CTTCCGGATC GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
 151 GACCAGGACT CGCTCAGCAG CAGCCTGAAA ACTTGCTACA AGTATCTCAA
 201 TCAGACCACT CGCAGTTTCG CAGCTGTTAT CCAGGCGCTG GATGGGGAAA
 251 TGCAGAACGC AGTGTGCATA TTTTATCTGG TTCTCCGAGC TCTGGACACA
 301 CTGGAAGATG ACATGACCAT CAGTGTGGAA AAGAAGGTCC CGCTGTTACA
 351 CAACCTTCAC TCTTTCTT ACCAACCCAGA CTGGCGGTTC ATGGAGAGCA
 401 AGGAGAAGGA TCGCCAGGTG CTGGAGGACT TCCCAACGTA CTGCCACTAT
 451 GTTGTCTGGC TGGTCGGAAT TGGCCTTTCC CGTCCTTTCT CAGCCTCAGA
 501 GTTTGAAGAC CCCTTAGTTG GTGAAGATAC AGAACGTGCC AACTCTATGG
 551 GCCTGTTCT GCAGAAAACA AACATCATCC GTGACTATCT GGAAGACCAG
 601 CAAGGAGGAA GAGAGTTCTG GCCTCAAGAG GTTGGAGCA GGTATGTTAA
 651 GAAGTTAGGG GATTTTGCTA AGCCGGAGAA TATTGACTTG GCCGTGCAGT
 701 GCCTGAATGA ACTTATAAAC AATGCACTGC ACCACATCCC AGATGTCATC
 751 ACCTACCTT CGAGACTCAG AAACCAAGAT GTGTTTAACT TCTGTGCTAT
 801 TCCACAGGTG ATGGCCATTG CCACTTGGC TGCCCTGTTAT AATAACCAGC
 851 AGGTGTTCAA AGGGGCACTG AAGATTCGGA AAGGGCAAGC AGTGACCCCTC
 901 ATGATGGATG CCACCAATAT GCCAGCTGTC AAAGCCATCA TATATCAGTA
 951 TATGGAAGAG ATTTATCATA GAATCCCCGA CTCAGACCCA TCTTCTAGCA
 1001 AAACAAGGCA GATCATCTCC ACCATCCGGA CGCAGAACATCT TCCCAACTGT
 1051 CAGCTGATTT CCCGAAGCCA CTACTCCCCC ATCTACCTGT CGTTTGTCT
 1101 GCTTTGGCT GCCCTGAGCT GGCAGTACCT GACCACCTCTC TCCCAGGTAA
 1151 CAGAAGACTA TGTTCAGACT GGAGAACACT GATCCCAAAT TTGTCCATAG
 1201 CTGAAGTCCA CCATAAAAGTG GATTTACTTT TTTTCTTAA GGATGGATGT
 1251 TGTGTTCTCT TTATTTTTT CCTACTACTT TAATCCCTAA AAGAACGCTG
 1301 TGTGGCTGGG ACCTTTAGGA AAGTGAATG CAGGTGAGAA GAACCTAAAC
 1351 ATGAAAGGAA AGGGTGCCTC ATCCCAGCAA CCTGTCCTTG TGGGTGATGA
 1401 TCACTGTGCT GCTTGCCTG CATGGCAGAG CATTCACTGC CACGGTTAG
 1451 GTGAAGTCGC TGCAATATGTG ACTGTCATGA GATCCTACTT AGTATGATCC
 1501 TGGCTAGAAT GATAATTAAA AGTATTTAAT TTGAAAAAAA AAAAAAAA
 1551 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA
 1601 AAAAAA (SEQ ID NO:1)

FEATURES:

5' UTR: 1-57
 Start Codon: 58
 Stop Codon: 1180
 3' UTR: 1183

Homologous proteins:

Top 10 BLAST Hits

		Score	E
CRA 108000024649260	/altid=gi 12734163 /def=ref XP_005134.2 farnesyltransferase 1	770	0.0
CRA 18000004925908	/altid=gi 4758350 /def=ref NP_004453.1 farnesyltransferase 1	743	0.0
CRA 18000004929946	/altid=gi 2135096 /def=pir I38245 farnesyltransferase 1	741	0.0
CRA 18000004993865	/altid=gi 2136196 /def=pir I52090 squalene monooxygenase	740	0.0
CRA 18000004932414	/altid=gi 6753838 /def=ref NP_034321.1 farnesyltransferase 1	671	0.0
CRA 18000004937535	/altid=gi 9506591 /def=ref NP_062111.1 farnesyltransferase 1	654	0.0
CRA 1000682330885	/altid=gi 6002565 /def=gb AAF00038.1 (AF09038.1)	582	e-165
CRA 335001098694081	/altid=gi 11514495 /def=pdb 1EZFA Chain A, farnesyltransferase 1	579	e-164
CRA 18000005103884	/altid=gi 2463565 /def=dbj BAA22557.1 (AB0022557.1)	282	1e-74
CRA 18000005103885	/altid=gi 7434086 /def=pir T00489 farnesyltransferase 1	280	4e-74

FIGURE 1A

BLAST dbEST hits:

	Score	E
gi 12926380 /dataset=dbest /taxon=960...	1441	0.0
gi 12945082 /dataset=dbest /taxon=960...	1370	0.0
gi 12921315 /dataset=dbest /taxon=960...	1346	0.0
gi 11642571 /dataset=dbest /taxon=96...	1330	0.0
gi 9141948 /dataset=dbest /taxon=9606...	1281	0.0
gi 13040072 /dataset=dbest /taxon=960...	1233	0.0
gi 12944143 /dataset=dbest /taxon=960...	1055	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12926380 placenta
gi|12945082 T cells from T cell leukemia
gi|12921315 Fetal brain
gi|11642571pancreas
gi|9141948 Burkitt lymphoma
gi|13040072 bladder

From tissue screening panels:

Whole liver

FIGURE 1B

1 MEFVKCLGHP EEFYNLVRFR IGGKRKVMPK MDQDSLSSSL KTCYKYLNQT
51 SRSFAAVIQA LDGEMRNAVC IFYLVLRALD TLEDDMTISV EKKVPLLHNF
101 HSFLYQPDWR FMESKEKDRQ VLEDFPTYCH YVAGLVGIGL SRLFSASEFE
151 DPLVGEDTER ANSMGLFLQK TNIIIRDYLED QQGGREFWPQ EVWSRYVKKL
201 GDFAKPENID LAVQCLNELI TNALHHIPDV ITYLSRLRNQ SVFNFCAIPO
251 VMAIATLAAC YNNQQVFKGA VKIRKGQAVT LMMDATNMPA VKAIYYQYME
301 EIYHRIPDSD PSSSKTRQII STIRTQNLPN CQLISRSHYS PIYLSFVMLL
351 AALSWQYLTT LSQVTEDYVQ TGEH (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 2

1	48-51	NQTS
2	239-242	NQSV

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 5

1	39-41	SLK
2	50-52	TSR
3	158-160	TER
4	313-315	SSK
5	322-324	TIR

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 3

1	81-84	TLED
2	145-148	SASE
3	147-150	SEFE

[4] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 2

1	137-142	GIGLSR
2	276-281	GQAVTL

[5] PDOC00009 PS00009 AMIDATION
Amidation site

22-25 GGKR

[6] PDOC00802 PS01044 SQUALEN_PHYTOEN_SYN_1
Squalene and phytoene synthases signature 1

128-143 YCHYVAGLVGIGLSRL

[7] PDOC00802 PS01045 SQUALEN_PHYTOEN_SYN_2
Squalene and phytoene synthases signature 2

164-189 MGLFLQKTNIIRDYLEDQQGGREFWP

FIGURE 2A

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	125	145	0.834	Putative
2	241	261	1.467	Certain
3	339	359	1.716	Certain

FIGURE 2B

BLAST Alignment to Top Hit:

>CRA|18000004925908 /altid=gi|4758350 /def=ref|NP_004453.1|
farnesyl-diphosphate farnesyltransferase 1;
Farnesyl-diphosphate farnesyltransferase 1 (squalene
synthase); Squalene synthase [Homo sapiens] /org=Homo
sapiens /taxon=9606 /dataset=nraa /length=417
Length = 417

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60
MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA
Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60

Query: 61 LDGEMRNAVCIYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ 120
LDGEMRNAVCIYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ
Sbjct: 61 LDGEMRNAVCIYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT----- YCHYVAGLVG 137
VLEDFPT
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTIVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEWSRYV 197
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEWSRYV
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEWSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELLITNALHHIPDVITYLSRRLRNQSVFNFCAIQPQVMAIATL 257
KKLGDFAKPENIDLAVQCLNELLITNALHHIPDVITYLSRRLRNQSVFNFCAIQPQVMAIATL
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELLITNALHHIPDVITYLSRRLRNQSVFNFCAIQPQVMAIATL 300

Query: 258 AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR 317
AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR
Sbjct: 301 AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR 360

Query: 318 QIISTIRTQNLPCNQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 374
QIISTIRTQNLPCNQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH
Sbjct: 361 QIISTIRTQNLPCNQLISRSHYSPIYLSFVMLLAALSWQYLTTLSQVTEDYVQTGEH 417 (SEQ
ID NO:4)

>CRA|108000024649260 /altid=gi|12734163 /def=ref|XP_005134.2|
farnesyl-diphosphate farnesyltransferase 1 [Homo
sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa
/length=431
Length = 431

Score = 743 bits (1898), Expect = 0.0
Identities = 374/417 (89%), Positives = 374/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 60
MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA
Sbjct: 15 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSSLKTCYKYLNQTSRSFAAVIQA 74

Query: 61 LDGEMRNAVCIYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ 120
LDGEMRNAVCIYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ
Sbjct: 75 LDGEMRNAVCIYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ 134

Query: 121 VLEDFPT----- YCHYVAGLVG 137
VLEDFPT
Sbjct: 135 VLEDFPTISLEFRNLAEKYQTIVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 194

FIGURE 2C

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEVSRYV 197
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEVSRYV
Sbjct: 195 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEVSRYV 254

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIHQVMAIATL 257
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIHQVMAIATL
Sbjct: 255 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIHQVMAIATL 314

Query: 258 AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR 317
AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR
Sbjct: 315 AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR 374

Query: 318 QIISTIRTONLPNCQLISRSHYSPYIYLSFVMLAALSWQYLTTLSQVTEDYVQTGEH 374
QIISTIRTONLPNCQLISRSHYSPYIYLSFVMLAALSWQYLTTLSQVTEDYVQTGEH
Sbjct: 375 QIISTIRTONLPNCQLISRSHYSPYIYLSFVMLAALSWQYLTTLSQVTEDYVQTGEH 431 (SEQ ID NO:5)

>CRA|18000004929946 /altid=gi|2135096 /def=pir||I38245
farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21),
hepatic - human /org=human /taxon=9606 /dataset=nraa
/length=417
Length = 417

Score = 741 bits (1893), Expect = 0.0
Identities = 373/417 (89%), Positives = 373/417 (89%), Gaps = 43/417 (10%)

Query: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSLKTCYKYLNQTSRSFAAVIQA 60
MEFKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSLKTCYKYLNQTSRSFAAVIQA
Sbjct: 1 MEFVKCLGHPEEFYNLVRFRIGGKRKVMKMDQDSLSSLKTCYKYLNQTSRSFAAVIQA 60

Query: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ 120
LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ
Sbjct: 61 LDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQ 120

Query: 121 VLEDFPT-----YCHYVAGLVG 137
VLEDFPT
Sbjct: 121 VLEDFPTISLEFRNLAEKYQTIVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVG 180

Query: 138 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEVSRYV 197
IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEVSRYV
Sbjct: 181 IGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWPQEVSRYV 240

Query: 198 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIHQVMAIATL 257
KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIHQVMAIATL
Sbjct: 241 KKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIHQVMAIATL 300

Query: 258 AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR 317
AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR
Sbjct: 301 AACYNNQQVFKGAVKIRKGQAVTLMDATNMPAVKAIYYQYMEEIYHRIPDSDPSSSKTR 360

Query: 318 QIISTIRTONLPNCQLISRSHYSPYIYLSFVMLAALSWQYLTTLSQVTEDYVQTGEH 374
QIISTIRTONLPNCQLISRSHYSPYIYLSFVMLAALSWQYLTTLSQVTEDYVQTGEH
Sbjct: 361 QIISTIRTONLPNCQLISRSHYSPYIYLSFVMLAALSWQYLTTLSQVTEDYVQTGEH 417 (SEQ ID NO:6)

FIGURE 2D

Docket No. CL001201DIV
Application Serial No. TBA
Inventors: Ming-Hui WEI et al.
Title: ISOLATED HUMAN ENZYME PROTEIN...

Hmmер search results (Pfam):

Model	Description	Score	E-value	N
PF00494	Squalene and phytoene synthases	425.8	4e-124	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00494	1/2	47	126 ..	1	88 [.	124.6	1.1e-33
PF00494	2/2	127	291 ..	146	317 .]	301.1	1.3e-86

FIGURE 2E

1 TATTTATTCC TAATTAATG GGGAGGAAAG TCTTGTAGA GGAACCTCTA
51 CTTTACTTTT TATACCGTCA TGGCTGGAAA CTAAGTTTTT AAGATTTTC
101 TGGGGTTCCC TTGGCCGAGG TGGGGAGTGG GAGGGCTGTC CAGTGGTAGG
151 GACTTAGGAT TTTTAGTTA CAGTAGTAGG GAAACACTC TGTAATCTAA
201 TACATAAGTA AATGATGTAT TAGAATATGG TAAATATAGG CAAGTAGACC
251 CCCACTGGGA TTAGCAGTGG TGGAAATGTG AGAGAGGGCA AACAGGTGGG
301 TCTAGATGAG GTGTGAGCAG ACTCGAGGGG CACAGGAGTT AGTCAAGCCA
351 GTATCTGGGG GATAGTGCAG GAATAGTGA CAGCTAGACA AAAAGTCCTA
401 GGGCCAGAGA AAGCAAAAGC ATAAGAGATG GAGGCCAGAG AGGTAATCTG
451 GGTGGAAGGC TGCAGCCCT CAGGATCCCT ATAGGTGCTT TGGCTTTGT
501 TGGAGAGACA CTGAACAGCT TTGGGCAGTG AACGTACCTG ACAGGTTCC
551 TGTTTGTGTT TGAGATGAAG TCTCGCTCTT GTCCCCCAGG CTGGAGTGCA
601 ATAGCGCGAT CTCAGCTCAC TGCAACCTCT GCCTCCTGTG TTCAAGCGAT
651 TCTCTGCTCAGGCCCTT CAGGCCCTCCA GGTAGCTGGG ATTATAGGCG CCTGCCACCA
701 TGCCTGGCTA ATTTTTGTAT TTTTAGTGA GACGCAGTTT CAGCATGTTG
751 GCCAGGCTGG TCTTGAACCT CAGACCTCAC GTGATCCGCC CGCCTTGCC
801 TCCCAAAGTG CTGGGATTAC AGGCCTGAGC CACCGCGCTC GGCTAGACCT
851 GACAGGTTT AAAAGGATTA CTGGTTGCTG TGTTAAAACA GACTGCAGGA
901 TGGCTTAGGT AGCCAGTAGG TTTTTTTTTT TTTTGGAGAC GTAGTCTTGC
951 TCTGTTGGAGT GCAGCGGTGT CATCTTGGCT CACTGCAAAC
1001 TCCGCTTCCC GGTTCAAGT GATTCTCCTG CCTCAGCCCT CGGAGTAGTT
1051 GGGACTACAG GCGCCCAACCA CCACACTCGG CTTTTTTGTAA TTTTTAGTAG
1101 AGACGGTTT CACCATGTTG GCCAGGATGG TCTCGATCTC TTGACCTCGT
1151 GATCCACCCG CCTTGGCCTC CCAAAGTGTG GCGATTACAG GCGTGAGCCA
1201 CCACGCCTGG ACGGGTAGCC AGTAGTTTCT AGGGCTGGAG AGATCTAGGA
1251 TGAGAGAACT TTCCACATTC CTGTTACAGG CTCTCTAAGG CTTCAAGCTCC
1301 TTTTCTAGG ACTAAGCTGG ATCTCAAGTA AACACTAGAG AGGGGGCAGC
1351 TGAAGCTCCA GGAGTGTGT GGGCTCCCTG GGGCTGGATG GCGGTGGCGG
1401 GCAGGCGAGC TGGCTGTGC TCGGGTGTGT TACAGTAAAG ACGCCCAGCT
1451 TGGCCTGCGC CCGCCCTTT CACGGTTTA GGCTCTACAG AGAGCGGCTG
1501 CAGAGCTCAC CCGGCTGGCA GGAGCCACCG AGGCCGGACA CGTGGGGCAGC
1551 TTATTGACCA AGTGGGGAGG AAGCAGCCCC GCACGTCTCT CCCGACTGCG
1601 GACCACCGTT GGGCTCATGC GCATCATAAG CCCCACCGCC TCACCTCCAG
1651 TCCCCACAGC GTTCGCGCTC CCAGCCGGGG TAAGCGGAAG AAAACAAAGG
1701 CCCGGCTCCA TCAGGGCACC AATCCGCTC GTCCGGCTCT TTCTCGGCCT
1751 CCAATGAGCT TCTAGGGTGT TATCACGCCA GTCTCCTTCC GCGACTGATT
1801 GGCGGGGTC TTCCCTAGTGT GAGCGCCCT GGCAATCAG GCGCCCGTCA
1851 GCCCACCCCA CGAGGCCGCA GCTAGCCCGG CTGGCGGCCG AGGCCGGTTG
1901 AAGTGGCGG AGCCGGCGGC GGGCGTCGC CGTACTAGGC CTGCCCCCTG
1951 TCCGGCCAGC CCCTCGAACG ACCTACTCCA CAGGTCCAGC CGGCCGGTGA
2001 GCGCCTGGGG ACCGCAGAGG TGAGAGTCGC GCCCGGGAGT CCGCCGCTG
2051 CGCCAGGATG GAGTTCTGTAA ATGCTTGTGG CCACCCCGAA GAGTTCTACA
2101 ACCTGGTGGC CTTCCGGAT GGGGGCAAGC GGAAGGTGAT GCCCAAGATG
2151 GACCAGGTGG GCGAGCCTC CCTGCTTGCC CGGGGGGGGG AAGGAGCTCG
2201 CTGGGCCGGC CTCAGGGCCT GAGCGCCGG GCCCAGGATCT GGGGCAAGGG
2251 GCGCCGGCGAG CAGGGCCGAC GCCTGGGTGT TCCCCTCCCG CTTCCTCGA
2301 GCCTCCCCC TGTAGGGCCC GGGTGGACGC GGGCGTCCCTG GCTGACCTGT
2351 CCCTGCCCCC GCAAGGCCGCTC CTGGGCATGA GCGACTTTTG CGTGGTTCCC
2401 GGTGGTTGCG CTCCCCGTTT CGTCCCCCTCC GTGAGCATCG GCGCTTACCG
2451 GTATTTAAC CCGAGGGTTA CACATCTGAG GCAATGTGGG TGGGTTACGC
2501 GGGAGAGGAC GAGTGAGTTT TTTGGTAAGC GGAATGAACAT ATGCAGATAA
2551 CATCACATGA AGGCCGTTTC TGGAATGAAG TCTGACTCCT CCAGTTTCAC
2601 CACCTCTTCC GGAGCTCTCC CGCCTTGCT GCCTTCCATC GCTTCATCCT
2651 CGGTGCTTCC TGAGTTTAA AATCGCCTAT CTACGCTTCC AAGTTCCAAT
2701 GAGTTATCTA ACGTCTATGG ATTAGCTAGG TGTTGGTGG AAGGTCAAGAA
2751 CTTGGTTTA CTTAGATTTT TATCTGCTCTC ATGCCGTGTAC TATTGTTTA
2801 ATGAATGCAT AGGAGGTGTT TTTATCCAA CAAGAAAATT ATTCGTACGC
2851 GATTATTGAA TGAATAGACA AATTCAAGCCA AGTTCTTCTG GTCTGGACCA
2901 GCCTGGCTGA TTTCTGTAAC TTTTTGGGC CAACAGGACA GTAGCAAATG
2951 TGACTCAGGC CGAGGCTGTA TAGGTGCCTG AACATCGGAG TCTTTCTTTC
3001 AGTGTCCATG TGCTTCAGTA AACACACTAG AAAATAAATT TCTGGTTTT
3051 GTCCCCAGTA GACTACACCC TCATTGGTG TTATTTTCA CGTGCTATCT

FIGURE 2A

3101 TTAATACAGG TACATCCTTC AGTCTATTG TAGAACATTC AGTTTCTTC
3151 ATCTTTCTT TGCCGGTGC ACATTATTG AATTATTTG CTACAGAATA
3201 ACTTCTATTA TTTGATATGG CAGATGTCAC TTTTTATATT TAGATATAGC
3251 ATTCATTTAT TTAACAAATA TTTGACGACC AGTTGTATAT CAGATAGTGT
3301 TCTAGGTGCT GGAGGTACAA CAGTGAACAA GCTAGGTGAA GACCTTGATT
3351 TTATAAAACT TACTTTTAG TGGAAAGAGAG ACAATTAAA AAAGCGAATG
3401 TACAGTTTT CACGTGGAGA AAAGCACTGC AGAGGAAGAT ACTAGCAGGG
3451 CAAGGGATCT GAGTGCAGTC AGACCTCATT TGGGTCCAGA CTTCATTCT
3501 CTATGTCTCT TTCTTTCTA CAGAAAGACT GTTAGAGAAA ATGGTAGCAT
3551 TGGTTTCTG TTGGGAGGGA AAGTGGGTGG TCATGGTAAG TGGGTAGAGA
3601 AAGACTTCAC AGTATACTGT TTTGACAT TTTGAGTTTT TTTAAAAGCG
3651 AGACTTGAGC TATTCTAGCT CTGATAATAT GGTGCAGTAT TTGTTATGTT
3701 AGTTGTAGTC TTTCTGGCA GTTTTACAT CCCCATGAGC CGTTAAAAAA
3751 ATACACTGAAC CTTTAATTAG GGGAAATAAA TTGGAAAAT ACATTTCCCT
3801 TCACTTAACA TTATCTTAGT TTCTCTTTT TTTTTTTTTT TTTTTTGAGA
3851 TGGAGCTTCTG CTCTGTTACC CAGGCTGGAG TGAGCTGGTG GCGGGACCTC
3901 AGCTAGATGC AGCCCTCCGCC TCCTGGGTT AAGCAATTCT CCTGCCTCAG
3951 CCTGCTGAGT AGCTGGGATT ACAGGGCACCT GCCACTACGC CCGGCTGATT
4001 TTTTGGTATT TTTAGTAGAG ACGGGGTTTC ACCATGTTGG CGAGGCTGGT
4051 TTTGAACCTCT TGACCTCAAG TGATCTGCTC GCCTTGGTCT CCCAAAGTGC
4101 TAGGATTACA GGCGTGAGCC ACTGCAACCCG GCCTTTTTTT TTTTTTTTT
4151 GAGGGGGGGG TCTCACTCCA TCGTCCAGG TAGAATGCTG TGGCCTGAAC
4201 ATGACTCACT CCAGTTTGAGA CTTCCTTGGC TGAAGCCATC CTCCCACCTC
4251 GGCTTCCTGA TCCCGAGTAG CTGGGACTCC AGGCACGTGT CACCAATGCA
4301 TGGCTAATT TAAATTTTTT TTGTAGACAC AATGTCTCGC TGCATTGCC
4351 AGGCTGGTCT TGAACACTTG AGCTCAAGCG ATTTTCCCAC CTCAGCCTTC
4401 AAAGTGCTGG GATTACAGGT GTGAGCCACT GCACCCAACC AGTTTCTCTC
4451 TGCAAACCTAG GGAAAAAATT TACGCTTAGC AGATATTGAG GGCTGATTAT
4501 TTCTATCACA GAAGCATTG GCTATAGAAT TTCAAGGGTTT AGTAAACTTG
4551 ATTTACACTG AATTTTAAAG TGCAATATCAG TAAATCTACG GGCATATGCC
4601 GCCTGCAAGT TGTGTGGCAT CACCCAAAAG CCGAGAGTAA TGGAAAGAGC
4651 AGGCTGTTAG TAATCAGGCA GATCTGGCTC CTGTCCAATC TAAATCCTGT
4701 TATTAGACT AATATCTAA GTCTGTTATT AAGTCCGATT TCTGACGCTA
4751 TTAAGTTAGG TGAACAAACCT TGGTAACCTA ACCTCTGAAC CACAGTTACT
4801 TCATCTGAA AATAGGGATG TATGTATGGT AACGATTTTT TAACCACAAAC
4851 TTCCCAACTC TAAGATGGTC TGAAAAGAAAT TTTTGAGTG TTTGGCTCAG
4901 AATCACTTGG CAGCAAACCC TGACTTGAAG TTGAGGCTTC ATTCACTCCA
4951 CTTAGTATAT TCAAATGTT TGCTAAAGAA ATAATTATGA GGTGCTACTT
5001 CACACTGACT AGGGTTGTAT ATGCATTTA TTGCCTATT TCTAAACAC
5051 TAAAAATGCT AAATTCTGCC CCAGGTCTTG CCACAGATGT TTCAGTGGAC
5101 TATGGGCTG TGAGACCTTA AAGGGTTGAT TGAGTAAGGA TCACAGGTGA
5151 TGTCCGCATT GTGCTTGGCA TGGAGTTAAG TGCTTGATAA ATGGTGGTTA
5201 TCAATCTGAT TATGTAATT TATGTAATT CAGTTCTCAA GTTTGTGGTT
5251 TTTTCCCTT CCTGGAGAAA TCTATTCTAT TTAAAGTGA GGAAGGCTCC
5301 GTGGAGGGCT GGTAGCTGGT AGCTGTTAC TTGTGGAACCT TTCAGCCTGA
5351 GGCTGGGCC CCTCCCTGG AGTCTGGTCT TGTGCTCTC CTGACCACCC
5401 CCACACCCCTT CCTCTAAATT CCCTCCATCC CTGTTTTCT CCCGCTTGC
5451 AGCTTTGGG AGTGTGCTGA ATCTCAGACT GCAATAGATA AACCCAAAGAG
5501 GGACAGGCAC CAGTAGCCTG AGCTTGTCTT CTCCCCCTGGC TCATGGGAAT
5551 CAAGCAGTAG AAATTTTTAG TGAGTGTGT TTTCCATAGT ATGCTTACTA
5601 GTTGTGTCTT CTCGTTTTGT TCTTGGTGAT TTGAAGAAAC CTGTTTACAA
5651 GGTAAAGGGAC TGAAACAAAT AGGTGACAGG AAAAAGAGCA GCAGGGGTAC
5701 GAGCTGGAGG AGTAAGTGGC TTGGCTTGCT CTCTTTCAGA ATGGAGGGCT
5751 GTATGGAAAG GAGGGGTAGT GTTCTTGAAG AGTGTGTTGGGG TTTAAATCTA
5801 GGGGGACCGT GTCTTGGCAT TGATTGAAAC TCTGGCTTA ACATCACCCC
5851 GAAACTGTTA GTTGGACTGA ACATGACATT TGGCAGTGCA GTTAAAACA
5901 CTTCTGCTG TAGCCTGGTA ATGGTCAGGC TATGTGAAGA GCTGCTCTGG
5951 AGCTCAGTCC AGAGCGGGTA TTCTGTTCTT TTCACTCTGA AATCCTGCCT
6001 CTCGATATT TGGAGAAGGAA GGAGTGGTG AATTGTTTTA AAATCCTCGA
6051 TGAATGTCTT CATTATTCA TGACACCACT TCTGAATATA TTTATGTGCC
6101 AGACGCTGAA GTTTACTAAT ATTATGGTGC CCAGTAAATA CTTGTTTTA
6151 CTAATATT TATGGCAAT AAAATGACTT TTTCAGGATT ATGTGATTAA

FIGURE 2B

6201 AAAGATTGAC CCTTTGGCA AAATACGTAT TCATGATAGG AAATATATAC
6251 AACATAGTTC ACTTAAACCT CCCACAGAG CCCAGGGTTC ACTGTTACCA
6301 TTCTGAAGTG ACTGGAATT CCTAGAAGTG GATATGCCAT ATTTTTTAA
6351 CCACTCCTAT TGGATATTG TTTTTTATT TTTTGAGATG GGGTCCCAC
6401 CTGCAGTGTAA CAATATCATA GTTCACTGTAA ACAGTGTATCT CTTGGGCTCA
6451 AGCGATCCTC CCCACCTCAG CCTCCCTGAG TAGCTAGTCT TCAGTAGCTA
6501 GACTATAGGT GGGCGCCACC ACAGCTGGCT TTTTAAAAAA TTTTTTATGA
6551 ACACGAGGTC TCACTATGTT GCCCAGGCTG CCCTCAAACCT CCTGGGCTCA
6601 AGTGAATTCTC CCACCTTGGC CTTCCGAAGT GCAGGGATTAA TAGGCGTGC
6651 CCACTGCACC CGGCCCTGTT GGATAAATGA TTCCAGTCTC TCCCCAAAAG
6701 AACCTGTTGTA AGACTGTGGG GTGAGGGGAG GGAAGGGACA AATAGGAACC
6751 CGCCGTATTT TCCACTCCCT GTGGGCCCTAA AACTGCTCTA AAAAATAGTC
6801 CATGAAAAAA TACATAGTAC AAACAGCAAC TCTTCTGTAT ATGCTTGCAT
6851 TTAAATCAG GCTTTTCTC CCTTTTGGAA AACACACAGTC CTTGTTGCT
6901 TTAGGGAAGA GTAAAGGTCA GTGCGCTGCA TTGCAATTAAAT TTGCAAGGGAA
6951 AAGATGAGAA GACATCTTGA AAGGAATGGC TTGCTTTCTA GAGAATAGTA
7001 GAGGCTTAAAT AGGTGTCATA GAAAACCAG GGTGGACAG TGGTAGTAAA
7051 ACCGCAAAAC AGATTTTATT CAGAAAAACT ACTGCAGTAA GAGGAGAGAG
7101 ACCTCGGTAC AGAACTGCTC CACTGCGAAT AAAAAGAAAA GTAGGAATTG
7151 ATGGCGGGGG AGCCGGATGT CAGTGGATGG AAAATTATTA CGAGGAAACA
7201 CAGGGGTGTG CATTCTTGTCT GAAGGCAGGC CAGAGTTATC AGACATCACC
7251 TGAGGGATGG AGGGGGATGT GGAACCTAAT CGGCTGTCTA GGGTGTATCAG
7301 ATACTGAAGT TGGGGGATTG TGGTCAAATC AATTAGCAG GATTCTTGGT
7351 AAAACTGGGC GATGCAAAGA CAGATGCGTT GAGTACAAAG TCCAGGCTT
7401 ATTGGGAAGA GGATTTCAAGC GGAGCCCGAG TAGAGTTTGG TCTAGGGAGA
7451 CTCTGTCACT GGGAGGACCA GCGAGCCGCT CGGAAGTGCCT CTGGGTTCTC
7501 TTAGCGGCCA GTGGGTTCTG GTGAGAAGGG CAACAGCGGG AGGAGGCGCC
7551 GGTGCGGGAGC GGGAGGCCGG GGGCGGGGCT GCGGGGCTGC GGGCGGGGCC
7601 CGTTGTGGGT CGGCCAGCG CGTATTGAG TAGAGGGCGA GCCCCTGCCG
7651 CCTCTCGTCG GGCGCTTCCC AGATCTGCTT GAGTCTATGG AGGAAAAC
7701 CGCGGGGTC CGCGATTCCC ATGGCCGCAG CGGCCTGCGG CACCAAGGCC
7751 ATGGCCCTCT TCAAGCGCAC CTTGGTGCTG AGTCCCAGCC CGGCGCCAG
7801 GGGCCCGGGC GCAGGCACCG CCCCAGGGGG CTGCTGCTT CCTCCTGCCG
7851 CCTGGCCCTG CAAGGACTGG CCTCGGGAG AGGGCGGCAG GCTGTGGAGC
7901 CGCCTGCCCC AGTCCCAGTC CCACTCCCAC TCCCACCTCCC ACTCCCAC
7951 CTGCTCCTCG ACGTCTCCC CCGCCGTGT TGTGTCTGC CGCAGGACT
8001 CGCTCAGCAG CAGCTGAAA ACTTGCTACA AGTATCTCAA TCAGACCAGT
8051 CGCAGTTCTG CAGCTGTAT CCAGGCCTG GATGGGGAAA TGCAGGTGAGT
8101 GATGGAGGCA GCGCTCTGG CTTGGAGGAA AGCTTGTCCG GGACTTTGA
8151 GTGTGTTGGA AGCTACCTTT TGATATAGCG CTCAGCGTT CAGCCTCGTT
8201 GCTGTGGCTT ATCCAGAACAA TAGCCCGGCC CTACGTGTTT ACTTTAGAAA
8251 GCCCTTCCAG GCTCTTGTCC ATCTAGTACA GTCCTGCGG GCCCAGCCTT
8301 TCAGAGAAGG GGGGGAGGG GGTGATGTTT ATTAACCTTT TTTAGTCTTG
8351 GCAGCTGAAC CTGCCTGTGA GCAGGCTGTG TATTTCTCGG CTTCCCTTAT
8401 CCAACTTGTG ATTTCTATTCT CTAGCATATT GGGTTGATTC TTTTGAAGCT
8451 GCCTCTGTGC ACATTACACC CATGAACCTTA GACCAGTTGC CTTTATGTAT
8501 GATCGTATT ATACTGAGAA GTTACTGTGT TTTTGACTT TCTTTCTAT
8551 TTGCTACATA TTAGTTCGGT CTAAACGTTT GGTCTTCTGG TCTCCATAGT
8601 TCTACATTGG TTAAATGCAA CTCACTTCTG GGAGTAGTGG TGACATTCAA
8651 CTAGTAGGCT TTTTAATAAA CTACAGAAGT TCATTACTCT CATGTAAGGA
8701 AGGAAAACAA ATGTAACCTT CGTTAAGTAT GAAAAGCGTT GGATATCCTT
8751 ATAGTTCTTT AGAGTAAAGG GTGAGATGGG TTTAGAAAGT GGCCAGGCC
8801 AAGTTATTTT AAAATAAAAA ATCTTGGCT GTTGTGTTCA ATATATTAAAT
8851 AGTTTCCCT TTTTACAGC AACGCAGTGT GCATATTTA TCTGGTCTC
8901 CGAGCTCTGG ACACACTGGA AGATGACATG ACCATCAGTG TGGAAAAGAA
8951 GGTCCCGCTG TTACACAAT TTCACTCTT CCTTACCAA CCAGACTGGC
9001 GGTCATGGA GAGCAAGGAG AAGGATCGCC AGGTGCTGGA GGACTTCCCA
9051 ACGGTGAGTG GGGTTACGCA TCTTGCTAC GGACTGTTGT GTTCATAATT
9101 GCTAACGTGG TTGTCCGGTA GCCTCCATAC ATGTGGAGAA AGGTTAAATA
9151 AGCATTCTGA GGGCAGCATA ATGTGAGGGT TAAAAACTCC GGTAGCCAAG
9201 ACTCTGAAGC CAGGCTGCCT GGGTTGGAAT CTAAATCTC CCACTTACTA
9251 AACTGTTGGT TACTTACAAA GACTCTCTGT GCCTCAGTTT CTTCATCTGT

FIGURE 2C

9301 AAAATAGGGG TAATAATAAC ACCTACCTCA TGGTATTCTG AGGATTCAAA
9351 GAATTAACGT AGGTAATGCT CTTAGAATGT TAGCTACTGC TGTTATTATC
9401 AGTATTGGAA GTCCAGTGT TCTTCCTGTG GGAAGACGCA GTCAAATTT
9451 AGTGGTGTGA AAGATTCTCA GGCTAGCTCA CAAAAGCCTG CCGACTGTAT
9501 GATGCAGCCT ACCTGTAAACA CTGCTGGCT CTTGACTACC CGGAGCCTGG
9551 TAGCATGGGA CTGCTGCTCA CGATGGCAG CAGCCTGGCA TGGGGGCGGT
9601 GTCTGTTGGC AGCTAGGGCG AGCCTGCG ACCCTCACCTG TGATCCTGGG
9651 CAAGTTCCCTT ATCTGCTTTG TGTCTCGTC TCCTCGTTTG TAAAGTTAGA
9701 GCTGAGAGGA TTAATTTCGC ACATATAAAG TACTTAGTGC CTGGTACAGG
9751 GTAAGTATTG TGTAAGTATT AGCTATTGG TCTATTGGT TGGAGTAAAG
9801 TGGGTTATAG TTAAAATCCT AAGATTTTA AAGTCCCTCA AGTTCACGTG
9851 GACATCTGCC TAGGTCCTAC TATCCTAGAA TTGCGATGTC TTATCACACA
9901 AATAACTGAT TCTTCCATAT CTTATAAATA AAGGTTGAT TTAGCAAAGT
9951 CACATGTTGT GAAATAGCTC GAAGAAGCCC TTTTGTCCA CAGTTGCCAG
10001 AGCTTTGGG GAACAGTCCT TATGTTATTG AAACAAACCT AATCTGTAGC
10051 TGAGTTGGG GGGAGCTAAAG TGGACAGAGA GTCCCTCCACC CAAACAAAAG
10101 AATCTTGAT TCTTGGGCAT AATGGGAGCA ATATTTAAAAA AAAAAAAA
10151 AAAAAAAA GGAATGTTG GGGAAAGACTC TTGCGGTGCA AAGGCTGTTT
10201 CAGATTGCTG AGATCAGACC TTAAGTACCA AAGCCCAAAT ATAGTACAC
10251 ATAATACAAA TGAGAAGAAA ATAGCTGAAG AATAATTGCA GTTATACAG
10301 TACAATTCAA GAGAAGAAAG AAAATTATG ACCACTAGCT GGGTGAGAAT
10351 TAGAACTGTA ACCCTGGGA GGTCTGGTG ATTGACTCT CACAGGACAC
10401 CTGATGACCA GAGGATGGGT TTCCCTTGT GGGAAATCTG TGGCGATTCA
10451 TTGATGGGCC TCTGAATTCT GCTGAAGCAG AGGAAGTAGT AATACCCAT
10501 TTATAATGGG AGTGCATTCT CACTTAAAAA CAACTAATAT TATTCTAGCT
10551 GGACCTAGCC TCTAGAAACA GCCAAATTAC ATTTGACTTG AGTGGATTCA
10601 TAATAATTAA AAAATTCTG GGGCATGGGA TAAATGTTG AGGTATTGCT
10651 AAGTCAAGGC AGCCCTATCC CCTCAGCAGA AGTGAGGGAA TATGAAAGTG
10701 TGTGAATGCT AACATAATT TGGGAATAT CGCCGTCAGA TTTCCAGATG
10751 ATATTCCAAC ATGTTGTGA AACTTCAGTG TCTTCCTGTG TTCATACAGT
10801 GTTCCAGTGG AAAAATAATG CTTAGTTCTG GAAGGTTCA GATGTAAACA
10851 CTGAACATCAT CGTTTCTTT TTTGGTAGT AGAGTTAGAG ATTCCATCCT
10901 CTTGAAAGCA CAGTTGCCCG GGGAAAGAGTA AAAGGGAGCA GAAGGCGTAA
10951 GCCAGGCACG GCTGTTTCA CTGTTGTC CTTTTGTAT CCTTACGAAT
11001 ATGAAGATGT ACTAAGTTGT GTGTTTGC TGATATATA ATTTTAAGCT
11051 ACTTGAGTTG TAGTCCCTC CAGTCTGTGA TTCAGTTGA GATGGGACTG
11101 TATGGGAATT AACAGTGCCT TGTCTCTTA AGCAGTGTGATT TGTGTATGTG
11151 CTGATATAGC TCAGTATGTC TTGAAACCA GTTGTCTGG GCTAGGCCTG
11201 CAATCAGCTT TTGGCTAAGA GGTCCAGGA TGAACAAGT AGTGTAAAG
11251 AGGACTGATA CCTTGGCCTC ACACACAGTA CTGCTCTTAG ACTGGGCAA
11301 GTGAAACTCC TCACTTCAGA GTGCCCTT CTAGGCCCCC TCACTCCCAA
11351 AGGGGTGAGG GATCACTGGG GCCATGGGA TGTGCTTGT CAGCTCTCGT
11401 GGGCTCTCCT TCTGTACCAAC GTTCTGGACA TCTGGAGTTC CTTGCCCCAA
11451 ATCCCTGAGC CCACGCTGTC GTCCGCACAG TCTATTCTCCT AAGGTCACTC
11501 CATCTCCTCC AGGTGGGAAC GTGCCACCAT TGACTGTGCC CTTGGCCTG
11551 AGTGATGGCC AAGGGCTGTG TTGGGGAGTG TTGTTGGATGG ATCCCTGGCAC
11601 CGAGGGCTGG GATATCTCT CAAATGAATG TGAGGTGCCT CCCAGTGC
11651 GAGAGAGCGG GATTCAAGGAA GCAGTGGAAAG GGAAGAGCCT GGGATATGGG
11701 GATCAGCTGT CTGTGCCCTG CTGCAATTCTG GAATAAAAAGT CTGAGGGACT
11751 AAGAATTCTA AATTCAAACCC TGAATCAACC AGGTTGTTAC AAAGATAAGT
11801 TTGTCAGTGC AGGAGGATAC AATATAATTG ACTTAAGTTA CTAGCTCGAT
11851 TGATCATTTT TAAATTTTTA GCTACATATA GTATGTGGC CTCCATTGTT
11901 CCTCTTATCC CAGGCCTTGC AGAATTAGG AATAAGCCTC AATACAGTGT
11951 TCTAACCCAG TGACTTCCCG CTCGATGTAC AGTAGATTGA ACCTGATCCT
12001 TTATACTTTA GTGATCATT GTTGTACCA GTTCAAGTCA GGCTTCTAG
12051 AAATCTCATT GTATGTTAGG GGTTCGATTA GAGTACAGTC ATGCATCACT
12101 TAATGAATGG CCACAGGATA CATTCTGAGA AACGCATTGA TAGATGATTT
12151 CATCATTCTG TGAACATCAT AGAGTGTACT TACACATACC AAGATGGCAT
12201 AGCTACTACA GACGTAGGCT CTGTTGTCAGG GGCATTGCT CCAAGGCTGC
12251 ACATCTCTAC AGGATGGTAC TGTAATGCAAT ACTGTAGGCA ATTGGAGCAC
12301 AGTGGTAAGT ATTTGTGTAT TTAAACATAG AAAAGGTATA GTAAAAACAG
12351 GGTGTTACAG TCTTAAGGGC CCACCATTTGT ATTTCAGTC TCCGTTGACT

FIGURE 2D

12401 GAAACATCAT TATACAGTAC ATGAGCACGT ATCTTTCTCA CCTGGTACTA
12451 GTGGAAAGCT AGAAGGCTTA GAAGTCTACC TGAAACATA GCTTAAGTAA
12501 TAATACAGCC TTATTTTAA ATGATAATAG CAAATAATAGT GTTCACTTAT
12551 TGAGCATTCT ACTATGAGTT ACTTACTAAA TATATTCAT CGTTAATTAA
12601 CTCTTGTGT TATTTGATCT ATAACATCGT TTAACAGGGA AATTACCTAG
12651 TACATAATGT ACTGTTATCT ACATTTTATC TAGATGAGGA AACTGAGGCA
12701 CAGAGAAATT AAGTACTTTG CCTAGGATTA CCCGTGAAGT TAAGTGACAG
12751 AATCAATGAA TCTGGAAGGT CTGGCTTCAG ATCTCTTGTG CTGAGTCACT
12801 CGCATACTTT ACTACCTCTA AGGTTCTAA TCAGAGGAAT TTGTATCTGT
12851 ATCCCTGCT ACTCTTACCC TCTATGTGGG ATTTGGCCTT TCTCCATTAT
12901 CCCTGTGAAC TCGCTCTGGG ACCTTCCTTC TTGTAATTGG AACCATCAGA
12951 AAGTGTACTG AGAACATAGA AATCTACTGT GTTGTGAAAC AGAATTACCT
13001 GGAAGCGGAA AAAGCCCTCC TGGCTCAATT CACATGTAC GGCTTATGGT
13051 CGTATCCGGG GAACATATGA AACTGGCAC TGAGTGCAGG GTCAGGAAAG
13101 CCCTGTCCAT CCTCTGGGTT TCTGGGAAA ACGTGGACCC CTTCATTGTC
13151 ACTTTCTCCT GTATAATTAA GTTTTACTT TTAGAACTGT ACAATTACGT
13201 AATAAATAAT AAAAGTCGT TGGAAGGATA GGTGAAGTTC AGAAGTAAA
13251 GTGTTTGGG GGAGTCTAAG CTCCCTCCCA CCCTCATTGA CCTTTCCCT
13301 CTAATAAAATA GAACGGTCT AACCAAGGAT CTGTGGAATG AGCAGAGTCC
13351 AACGGAGATT CAGGGATTCT AATAACCTCT TGTAGAATCA CTGGTTGTT
13401 TCAGCCACAA GAAGGAATT CCTTTGACA TTGGCTTGAA CAGCTGTTGT
13451 GCAAAGAAA ACTTTTGGG AAGTTCTGGA AGTACCAAGAT TGATTTATA
13501 GGTTTTTTTTT TTTTTTTTTG GAGGGACATG GGGGTATTGA CAGTTGATGT
13551 TAATCAGAAA TCCTAAATTG TGTGTATTCC TGGTATGTTG CAATCAGCCG
13601 GCCACCTGGT TTTCTCTGG GCTCTTAATT TTAGGTGTAT TCCGAGGAAG
13651 TTTTCTAAC TTTTCTGTAA ACACAGACCA GTTATATTGC ATACTTCAA
13701 TGTTTAACCA AATCTCTCA CTGTTGAG TATTATCTGT AGGCTCTCAT
13751 GTTTAAGAC TTCCCCATGG TGTTTTGTG TTGTTATTTG CTAACCTATA
13801 ACAATTCTT TGAACTTAA ACAAGATATT TGGGCAGTAA CAATAAATT
13851 TAAAAACATC AATTCAACTT TTTTACATTA GGGCTTGGAC TATGGAAAAA
13901 GTATTGGCA GCATGCCTCA TACTGAGTTG TTTAATGAAT TTAAAAGTAT
13951 AGCCNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14001 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14051 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14101 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14151 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14201 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14251 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14301 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14351 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14401 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14451 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14501 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14551 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14601 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14651 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14701 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14751 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14801 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14851 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14901 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
14951 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15001 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15051 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15101 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15151 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15201 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15251 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15301 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15351 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15401 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
15451 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN

FIGURE 2E

15501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
17551 NNNNNNNNGT GGAGAGTTCT GTAGATGTCT GTAGGTCTG CTTGGTCCAG
17601 AGCTGAGTTC AAGTCCTGGA TATCCTTGT TACCTTTGT CTTGTTGATC
17651 TATCTAATAT TGACAGTGGG ATGTTAGACT CGCACACAAT AATAATGAGA
17701 GACTTTAAGT CTTTTTCTAG GTCTCTAAGG ACTTGCTTTA TGAATCTGG
17751 TGCTCCTGTA TTGGTACAT ATATGTTAA GATAGTTAGC TCTTCTTGT
17801 GAATTGATCC CTTTACCAATT ATGTAGTGGC CTTCTTTGTC TCTTTGATC
17851 TTAGTTGGTT TAAAGTCGT TTTATTAGAG ACTAGGATTG CATTCCCTGC
17901 TTTTTTTTTT CGCTTGGTAG ATCTTCCCTCC AGCTGTTTAT TTTGAGCCTA
17951 TGTGCTATCTC TGACAGTGAG ACGGGTCTCC TGAATACAGC ACAGTGACGG
18001 GCCTGACTG TTTATCCAAT TTGCCAGTCT GCGCTTTTA ACTGGGGCAT
18051 TTAGCCCACT TATATTTAAG GTTAATATTG TTATGTTGA ATTTGATCTG
18101 TCATTATGAT GTTTGCTGGT TATTTGCCCTT ATTAAATTGAT GCAGTTCTT
18151 CCTAGCCTCG ATGGTCTTTA CAATTGGCA TGGTTTGCA GTGGCTGGTA
18201 CCAGTTGTTTC CTTTCCATT TTACTGCTTC CTCAGGAGC TCTTTAGGG
18251 CAGGCCCTGGT GGTGACAAA TCTCTGAGCA TTGCTTGTC TGTGAAGGAT
18301 TTTTATTCTC CTTCACTTGT GAAACTTAGT TGGCTGGTT ATGAGATTCT
18351 GGGTTGAAAA TTCTTTAAGA ATGCTGAATA TTGGCCCCCA CTCTCTTCTG
18401 GCTTGTAGGG TTTCTGCTGA GAGATCTGCT GTAGTCTGA TGGGCTTCCC
18451 TTTGTGGTA ACCCGACCTT TCTCTCTGGC AGCCCTAAC ATTTTTCTC
18501 TCATTTCACAC GTTGGTGAAT CTGACAATT CGATCTGG GATTGCGCTT
18551 CTCGAGGAAT GTCTTGTGG TGTTCTCTGT ATTCTCTGAA TTTGAATGTT

FIGURE 2F

18601 GACCTGCCTT GCTAGGTTGG GGAAGTTCTC CTGGATAATA TACTGAAGAG
18651 TGTGTTGAA CTTGGTTCCA TTCTGCTAT CACTTCAGG TACAACAATC
18701 ATAGCATTGG TCTTTTCACA TAGTCGCATA TTTATTGAAG CCTTTGTTCA
18751 TTTCTTTCA TTCTTTTTC TCTAATCTTG TCTTCTTGCT TTATTTCATT
18801 AATTGATCT TCGATCACTG ATATCCTTTC TTCTGCTTGA TCGAATCGGC
18851 TATTGAAGCT TGTGTTATGCT TTGTGAAATT CTTGTACTTT GGTTTTCAGC
18901 TCCATCAGGT CATTAAAGCT CTTCTCTACA CTGGTTATTG TAGTTAGCCA
18951 TTTGTCACAC CTTTTCTCAA GGTTTTAAGT TTCCCTGCGA TGGGTCAGAA
19001 CGTGCCTGCTT TAGCTGGAG AAGTTGTTA TTACCAAACCT TCTGAAGCCT
19051 ACTCTGTCA ACTCGTTAAA CTCATTGTCC ATCCAGTTTT GTTCCCTTGC
19101 TGGTGGAGGAG TTACGTTCT TTGGAGGAGA AGAGGCGTTC TGTTTTGGA
19151 ATTTTCAGCC TTCTGCTGT GGTTTCTCCC CATCTTG TGTTTATCTA
19201 CCTTGGTCT TTGATTTGG TGACGTACAG ATGGGTTTG GTGTGGGTGT
19251 CCTTTTGTT GATATTGATC CTATTCTTGT GTTTGTTAGT TTTCTTCTA
19301 ACAGAGGCC GTCAGCTGCA GGTCTGTTGG AGTTGCTGGA GGTCCACTCT
19351 AGACCCCTGTT TACCTGGGT TAACCAGTGG AGGCTGCAGA ACAGCAAATA
19401 TCGGGCCCTG ATCCCTCCTC TGGAAGCTTC GTCCAAGAAG GACACCCACC
19451 TATATGAGGT GTCTGTCGGC CCCTACTGGG AGGTGTCCTC TCCCAGTCAG
19501 GCTACATGGG GCTCAGGGAC CCACTTGAGG AGGCAGTCTG TCCGTTACTG
19551 GAGTCAAAT GCCGAGCTGG GAGAACCACT GCTCTCTTCA GAGCTGTCAG
19601 GCAGGGATGT TAAATCTGC AGAACCGTC TGCTGCCCTT TGTTTAGATA
19651 TGCCCTGCC CCAAGAGATGC AATCTAGAGA GGCAGTAGGC CTTGCGGTGG
19701 GCTCCACCCA GTTCAAGCTT CCTTGCTGCT TTGTTTACAC TGTGAGCATA
19751 GAAAGTGCCTA CTGAAGCTC AGCAATGGCG GGGAGGGCGCT TCCCCTCACC
19801 AAGCTCCAGC ATCCCAGCTT GATCTCAGAC TGCTTGGCTA GCAGCAAGCA
19851 AGGTTCCATG GGATGGGAC CCCCCGAGCC AGGCACTGGA GGCAATCACC
19901 TGCTCTGCCA GTTGCAGAGA CTGGAAAAG CACAGTATTT GGGCAGAGTA
19951 TACTGTTCTT CCAGGTACAG TCACTCACGC CTTCCTTGG CTAGGAAAGG
20001 GAAATCCCCCT GACCCCTTGC ACTTCCTGGA TGAGGTGACG TCCTGCCCTG
20051 CTTGGCTCA CCCTCCATGG GCTGCACCCA CTGTCACCAAG AGTGCCTAATG
20101 AGATGAACCA GGTACCTCAG TTGGAAATGC AGAAATCACC CATCTCTGC
20151 ATCGATCTTG CTGGGAGCTG TAGACCAGAG CTGTTCTAC TGGGGCATCT
20201 TGGAAAGCAAC TCTGGGCTG AGTTTCTGTT TGTTGCCCTG ATGTATATCC
20251 CCAGTGCCTA GAATGATACT TGTTACATAG GAAGTGCCTG ATCCATGTTT
20301 GCACAAATGA ATCTTTCTCA TAATGAGGTT TCTCTAAACA AGCTGTTCTC
20351 CCAAAACTT ACACCCAGT TTATGTTGAA GCATCTCATT ATACATTGGA
20401 AAGATGAAAT GTGTAGTGAG ACTTTGAATC TTCTTTGAA TCTAGAAACA
20451 TTAGCATTTT TAGCACATT TATTTTAATA TTTATGAAAT TTATGAAATA
20501 ATAAGAAACA TGAGGCCGG CTCAGTGGCT TATGCCTGTA ATCCCAGCAG
20551 TTGGGAGGC CAGGGCTAGT GGATCATGAG GTCAAGGAATT TGAGACCAAGC
20601 TTGGCCAACA TGTTGAAACCC CCACTTCTAC TAAAAATATA AAAATTAGCT
20651 GGGCGTGGTG GTGCATGCCT GTAATGCCAG CTCCCTGGAGA GGCTGAGGCA
20701 GGAGAACAT TTGAACCTGG GAGGGGGAGT TTGCACTGAG CTGAGATCGT
20751 GCCATTGCAC TCCAGCCTGG GCAACATTGC GAGACTCCAT CTCAAAACACA
20801 AAAACAAAAA CAAAAAAAT GTGTGACCTA AATTAGGCTT ATAGATGAAC
20851 CATTGCACTG ATGATTAATT CCGCCATTGT TTGCTTGTG ATCTTGGTG
20901 CCATGCTGT ACATATTCA TGATTTCTGT GTTTTACGG TTTCCATTTC
20951 AGATCTCCCT TGAGTTTAAAGA AATCTGGCTG AGAAATACCA AACAGTGATT
21001 GCGGACATTG GCCGGAGAAT GGGCATTGGG ATGGCAGAGT TTTTGGATAA
21051 GCATGTGACC TCTGAACAGG AGTGGGACAA GTTGTAGTCTC ATAAAACAGT
21101 GTCTGTTGTG GATGTATTAG ACAGAGCTGG CAGTCCTCAT AGTGAAGCTC
21151 AGAACAAAGAA AAGTTGTCGA GTATTTTCAG CCCCTCTGGT TTTACAATT
21201 ATCTGTTTAG GTTGAATGTC TCATCATAAA CAGTTTATTG CAGAGTTAAT
21251 TCCAAACAG CAGCTATGTA GGATATCAGC CAGGCTAGGA GTAGGGTACT
21301 GGAGAGAAAGT GCTTATCTAG ACAAAAGGGAT GTAATTGACC ATGAAGATTA
21351 AAAACTACACA TCAAAACATA AGGTAGGGTT AGGAGTCTTG CCTATTTTC
21401 ATAGGAATGG TGTTGTTGAG ACTTACTCAT CACTTCTGTG GAAGTAAAGA
21451 CATTTTATTT ATTATTTTTA AAGCCAGTCA GATTTAGCAG GCAGAGACAT
21501 TTCAGACATC TAAAGTGTG ATGTATTTCA TACCTTTAAC TGTGCTTAAA
21551 TTAGGATCTC CGAAAAGATG CTGCTACATG GTCACTACGT TAGTGTAGGT
21601 CCAAGGTCTT GGGCCTTAA ATTTCCTAAA CCTCAAAACT TGACAGCACT
21651 TATCTTTGGA ACTGCTGATT TGTGCTTCTT AAGTTAACAG CATAACAATGA

FIGURE 2G

21701 CTGCTAGAAA TCAATTCTG CATTAAAGGT GAAGTTAGCC GGGTACTATG
21751 GTTACCTGT AATCTCAGCA CTTTGGGAGG CTGAGGTGGG AGGATCATT
21801 GAGCCCAGGA GTTAGACACA AGCCTAAGCA ACATAGCGAG ACCCCGTCTT
21851 TCAAAAAATT AAAAATGAG CAGGGAATTG GTGGCATGTG CCTGTGGTCC
21901 CCAGCTACTC TGGAGGCTGA GGTGTGGAG GATTGCTTGA GCCCAAGAGT
21951 TGAAGGTTGC AGTGAGCCAT GATTGTGCCA CTGCACTCCA ACGTGGGTGA
22001 CAGAGCAAGA CACCTACTGA AAGAAAATAA AGTTGAAGTT AAAACTTCTG
22051 GCCAAGAACC AGCACTGGTT ATGATAGTAA CTCATTTCT GTTGTGCAGA
22101 TTTATTTCAGG AAACCTAATT TTAGGTTGTT GAATAGAAGT TTTGATCAGA
22151 TAAAATTGAA TTAAAAAAA TTTTTTTGAA GACAGGGTCT TGCTGTTATC
22201 CAGGGCTGGTG TGTAGTGGTG TGATCACGGC TCCCCCGCAGC CTCAACCTCC
22251 TGGGCTCAGG TGATCCTCCC ACCTCAGCCT ACCGAGTAGC TGTAACTACA
22301 GTGCATGACA CCATACCAGG CTCATTTTTG TACATTTTT GTAGAGAGAG
22351 GGTTTTGCGA TTGTTGGCCAG GCTAGTCTCA AACTCCTGGC ATCAAACAGT
22401 CCTCCCACTC TGGCCTCTCA AATGTTGGGA TTACAGGCAT GACCAGCCAA
22451 TTATTCAG GAGTTATTTT TTTTCTCTA CTTTGGGGGA AGATGAATTAA
22501 TATAAGTCTC CATTAGGAA GTATTCTAC CAAAAGAACT ATTATCTTCA
22551 AATATTTTTT TGGATAGTAC TATAGATATA CTAATTTTTT TTTAAATTTC
22601 TAGTAATTCT TTTGAAGATT TTGTATAGCT GTCCAAAGCC AATTTCCTGTC
22651 TACCTAATTCT CAGCAAGATT TCACTCTTT CATGTTACTT TTGTCAGA
22701 ACAAAATTCA AGTGCCTTCT CTTCACCTGT GCATTCTTCC CCCTGATTAG
22751 TCTCTGGCTT TGTATTACTT TCAGTCAGAG ACCACTTTTTT TTTTTTGAGA
22801 CAGGGTCTCA CTCTGTCACC CAGACTGGA TGCACTGGCA CAGACAAGGC
22851 AGCCTTGACC TTCTGGGCTC AAGCAATCTT CCTTGCCCTC AGCCTCTG
22901 GTAACTGGGA CCACAGGCAC GTTGCCACCA TGCCCTGGCTA ATTTATTTTA
22951 ATTTTATTAA TTTTGAGAC AGGGTATTGC TCTGTCAACCC AGGCTGGAGT
23001 GTAGTGGCAT GATCAAGGCT CACTGCAGCC TTACACCTCCT GTGCTCAAGC
23051 AGTCCTCTCA CCTCAGCCTC CCCATTAGCT GGGACTATAG GTCCACACCA
23101 CTACACCAGG CTAATTTTG TAATTTTTG GTAGAGACAG GGTTTCATCG
23151 TGTTGCCTAG GCTGGTCTTGC AGCTCCTGGG CTCAAGCGAT TCACCTGCCT
23201 TAGCCTCCCA GGTGTGAGCC ACTACACTCA GCCTTTTAAA ATTTTTTACA
23251 GAGATGAGGT CTTGCTTTGT TGGCCAGGCT GGTCTAAAAC TCTTGGGCTC
23301 AAGCAGTCCC CTCTCCACAG CCTCCAAAAA TTCCGGGATT ACAGGCGTGA
23351 ACTTCGGTCA TTTCCTTAAC TTTACCCCTTC CTAATGACAC TCCAGAGCTT
23401 ACCTCTTTA CTTTGCTTC TTAAGTTAAC TAATAGACAA TTATTGTATG
23451 TGGATATTGC ATTAAGTTGT CTTAGGATAC CCTTTTCAGA GGAGGACAGC
23501 TTTTGACAAA TTGCTGTCGC GGAAAAAAA AGTATTGAGC AATTAAGAGT
23551 TGCACTTACT GAAATCTCTG TTGAGAGAGG GGAAGTTACG TTGTCTCTAA
23601 AAGAAAAACT AAAAGAAAAA GGGGAAGTTT TAGCAAAGTT GTTAAAGCCT
23651 GACACTTAAG TCATACTACC TAGTTTGAA CTCTTAGCCC CTGCCACAGA
23701 CACGGCAGCC CTTGAACCT TCCTGGGTTA AAGCGAGCCT CCTACTTCAG
23751 CCCCCCTGAGT AACTGGGAC ACTGGCCTGT GTCACTGTGCT CGGCTAATT
23801 TTTTTTTT CTCACATGG GCAATGTTGG GCAAGTTAAA TCGACTTCTT
23851 TGTGCCCTAG TTTCTCATC TGAAATGGAG ATCATACTGC TATGTACCTG
23901 ATACAATGTT TGTGAGGATT GAATGTGCAG AGTTCTTTT TTCTGTTGTT
23951 GTTGTGTTGA GACGGAGTCT CACTCTGNNN NNNNNNNNNNN NNNNNNNNNNN
24001 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
24051 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNA TCTCGTGATC
24101 CGCCCGTCTC AGCTTCCCAA AGTGCCTGGG TTACAGGCAT GAGCCATCGT
24151 GCCCCGGCTGA ATGTGCAGAG TTCTTAAAC CGTGTCAAGA ACATAAAATA
24201 GTTATTGTT CTTTCATATA ATGATGATTT TGAGGGCCTG CGGATCTTGA
24251 CATGTTATCA GATTGGTCAA AAAAGATTA AACCATAGTT GGTATTGTCC
24301 TAGTCCCTGT TACCAAGATA TTCCCATCTT CATCGTTGCC TTCTCTCATA
24351 GTTTTATGTA TCAAAAGTT TATTGAAAG CTAGGCCGGG CACGGTGTCT
24401 TGGGCTGGTA ATCCCAGCAC TTTGGGAGGC CAAGGCTGGC AGATCAGTTG
24451 AGGTCAGGAG TTGAGACCA GCGTGGCCAA CATGGTAAA CCCCCTCTCT
24501 ACTAAAAATA AAAAATTAGC TGGATGTGGT GGTGGGTGCT TTAATTCCAG
24551 CTACTCAGGA AGCTGAGGCA GGAGAACAC TTGAACCCAA GAGGCAGAGG
24601 TTGCACTGAG TTGAGATTGT GCCACTGCAC TCCAGGCCAG GGGACAAAGT
24651 GAGACTTGAT CTCAAAAAAA AAAAATGAG AAAGTTATTG TAAAGCTAGA
24701 CACGGTGGTA TTGCTTACA ATCCCAGCTG TTGAGGGAAAGC TGAGGCAGAA
24751 AGATTGCTG GGTCCAGTAG TTTGAGTCTA ACGTGGGCAA ATATATGAGA

FIGURE 2H

24801 CTCCATCTCA AAAAAAAA TAAAAAATAA AAATAAAAAA ATGTTTACTA
24851 GTTTTTTC A GTAGCCTTT ATTATAGTAG CAGTACATGT GTATTGTAGA
24901 AATTGGAA ATACAAGTGA AAAATAAAA CATCAAATTC CCGTCAGCCA
24951 GAGACTGCTG TGAAATGTT TGAGCACATC CTCTTGAAT GTTTTTAAA
25001 TCCTGGTATG TATATTTGTA TTTTAAAATC AAAATGCATT CTTACCCATT
25051 CTCTTTGAA CCTGCTTTTG TGAGCTAAT GATCTCTAGT GTGTCCATT
25101 CAGTAAAAT TCCATTATTA AAGTGTCTTA AAAATCGTCT CTTACAGTAC
25151 TGCCACTATG TTGCTGGCT GGTCGGAATT GGCTTTCCC GTCTTTCTC
25201 AGCCTCAGAG TTTGAAGACC CCTTAGTTGG TGAAGATACA GAACGTGCCA
25251 ACTCTATGGG CCTGTTCTG CAGAAAACAA ACATCATCCG TGACTATCTG
25301 GAAGACCCAGC AAGGAGGAAG AGAGTTCTGG CCTCAAGAGG TAACAGATTC
25351 AGGGTATTTT GGGGGAAAAT AACTTTAGAC ATTCTCTGAA AAATCCTTA
25401 ACTCTTGTGG TTGCGGTGA CAGAAAACAA AGCCAGGCCT CCCCCAGGCA
25451 GCATAAGGGG ATGTGGAAA TAGGATAGAT TGACATGAGT TTGCTTCAGG
25501 TAGACTGGCT GACTCCCAGG ATTACACCCA CGTAATCAGT ATATTCAAGC
25551 CTTGCTGTCT TTGATTTCTT TCAGACGGTC TTCTCCAAG TGGTGGATAT
25601 GGTAACAAACC CACGTGCACT AGCTTAACAA AAAGTTCTTA GGAATGGCTT
25651 TGTTCCGGCT GGCGCAGTGG CTCATGCCCTG TAATCCCAAC AGTTTGAGAG
25701 GCCAAGGTGG CGGGATCACC TGAGGCCAGG AGTTCGAGAC CAGCCTGGCC
25751 AACATAGTGA AACCCCGTGT TTACTAAAAA ATACAAAAT TAGCCGGCG
25801 TGGTGGCAAG GGCTTGTAAAT CCCAGCTACC TGGGAGGCTG AGGCAGGAGA
25851 ATCGCTTGA CCCAGGAAGC AGAGATTGCG GTGAGCTCAG ATTGTGCCAC
25901 TGCACCTCCAG CCTGGGCGAC AGAGTGAGAC TCCCTCTCAA AAGAAGAGGA
25951 AGGGCTTGGT TCTTCTGCTC AGCCCTGAAT CAGTTACTGT TGCTACACAG
26001 CTGAGTTCTC TGGCCTCACCC TGATTACGT CTACACAGTA CACACAGAAT
26051 GGATTTCCCC CAAAGAAAAG ATTCTGCGGC AGGAAGGGGA AAGGGATGGC
26101 AGGTAGACAA AAACCTCCAGG TGTCTGTAAT AAGGGACAGG GTGATCTTT
26151 ATTAAAACA TGGACAGGGG ACAGAAAGCT TTGATACTG ATTTGTTCA
26201 GAAGGAAAGT AGAAAATTTT ATGACTGTT CCTGAATTAA TTCCAGCATT
26251 TACCTTTGC TTTCCATAAA AGTGTTCCT GCAGCCAAGT ACTTTAAAGT
26301 TTAAAGA CGGGTGAGGC TAAGTGTGGT GTCTCATACT TATAATCCCA
26351 GTGCTGAGGC CAGGAGTTCA AGACCAGCCT GAGCAACACA GCAAGATACC
26401 ATCTCTATAA AAAATTGTTA GAAAATGATT CTGCTGAAAG AGCAAAAATA
26451 AAAATTAAAG AAAGTAGAAA AAATAAAACT AAATTAAAAA GATTAACCTGG
26501 GCATTTGGC ATGCACCTGT ATTCCCTAGGT ATTCTGGGAGG CTAAGGCACA
26551 AGGATCCCTT GAGCGCAGGA GCTCAAGGTT GGATTGAGTT GTAATCACAC
26601 CACTGCACTC CAGCCTCGGT GGCACAATGA AACTGTCTCA AGAAAAAAA
26651 AAAGTGACAG AGGGAAACAA TATTGCAAT TCATAGAGCA GATACAGGGT
26701 TCATATTCCCT AATATTAAAAA AAAACTCTA AAAGTTAAGA AAAAGGCCAA
26751 CTGCCCCACA GAAAATGGG CAAGGAGATA AGAACAAAGAT TGTTCACAGG
26801 AAGAGACACA CAGATGATTA TTAAAAATCT GAAAAGATGC TGAGTCTTAC
26851 TCCTAAGAAA AATTCACTT TAAACTACTC TGGGGGCTGG GCAAGGTGGC
26901 TCACGCTGT AATCTCAACCA CTGGGAGACC AAGGCAGGAA GATCACTGAA
26951 GCCAGGGTAT CGAGACCAGC CTGGACAACG TAGTGAGACC TTATCTCTTA
27001 AAACAAAACA AAACAAAACA AAACAAAAAA AACAGTAAAA ATTGGCCGGG
27051 CACAGTGACT CCTGCCTATA ATCCCAGCAC TTGGGAAGC CCAGGTGAGT
27101 GGATCACTTG AGGTCAGGTG TTGAGAACCA GCCTGGCCAA CATGGCAAAA
27151 TTCCGTCTCT ACTAAAATTA CAAAATTAG CCAAGTGTGG TGGCATACGC
27201 TGGTAGGGCC AGCTACTTGG GAGGCTGATG TGAGACTCCA TTTAAAAAAA
27251 AAAATCAAA AATTAGCTGG GTATAGTGGC ACACCCCTAT AGTTCTCGCT
27301 CCTTGGGAGG TTGAGGCAGG AGGATTGCC GAGCCCAGGA GTTCAAGGCT
27351 GCAGTGAACC ATGATCACAC CACTGCATTC TAGCAGCCTG GGAGACAGAG
27401 CAAAACCCCTT GTCTAAACAA AAACAAACAA CAACAAAAC AAAAACACT
27451 TCCCTCAGCT CAGACATGGC CTTTTAAGTT TCCTAGGTGA CTCGTGTGCA
27501 GCCAGGGTTG AGAAACCACT CTTGTCTTAC CCCTTTTG CAGACACAGG
27551 GCTCAGAGAA GGGAAAGGGGA TTGTCTGGGG ATGTATAGTG AGGCAGTGGC
27601 TGCCTTGGAA GTGGAGTCTC AGTCTCCCGG CTCTTAGGCC AGCCCCCTGAC
27651 CACTGTTCCA TTGCTCTCCA GACAGAACAT CAGCCACGGG CATGTGATGC
27701 ATGAGCGTGA GCCACACCAT CTTGCACACA CAGGAGCAGA GCCCTGCTCT
27751 TCTCATTACAC TTACTTTATC TGTAATAG CATCATTCT ACCACACGGT
27801 GGTGGTGTGA ATAAAATGAG ATGAACTTCT AGCATAGAGT GCTTAGTAA
27851 GGTTCTGGAC ATTTCTGAGT AGTTGAATCA TGCCAAATGT GGTCCTAGGT

FIGURE 21

27901 GATTGGCTTC TTTTGCTAGC ATGTTTCAG GGCTCCTCCA TGCTGGGC
27951 TTGCATCACT GCTTTATTCC TTTTTATCGC CTAGTATTAT TCCACTGTGT
28001 GGATAGACCA CATTATCCA TTCATCAGTT GGAGGATATT TGGGTTCTTC
28051 CCATTTTTT TGGCTATGGT GAATAGTACT GTGTACATT GCATATAAGG
28101 TTTTGTGTAG ATGTGTGTTT TCCTTTTCT TGGGTCTATG CTGAGAAGTG
28151 GAATTGCTGG TTCATACAGC AGCTCGAAC TTGTGAGGAG CTGCCAGACG
28201 CTTTTCCAAG GTCGCTCAC CATTATACAT TCCCAGTCAGC AGTGTGAGAG
28251 TCCCAGTTTC ACCAGCACTT GTTGTATCT CTTTTTAACT GTATGTATAT
28301 ATACTTAACA TTTTATTAT AATAAATGTA CATAATAGAG AATTGCCAT
28351 TTAACTATT TTAAAGTCTA TTATTCAAGTG GCATTAAGTA CATTAAATGAT
28401 GTTATATAAC CATCAACACT ATGTTTCAG AACTTTCGCT AGCTTCAGAG
28451 AATCCTCTAA ATAATATCAT TAAAATCAT CAAGCCGAAT CCCACTGTTA
28501 GAATTAAAGG TTTTATTTCAG CTTTCAGTT ATCAGGATCC AGGGAGGTGT
28551 AATAACATTA GAGGATAGAC TCAGCTCATT TCCCAGCTAT GCCTTCAGC
28601 AGCATTCTTA CCAGAGTAGG AATATAATGT TAGTCATTAT TTAGAGGCCT
28651 GGCCATCTTG AGAAGGTTTA CTGTTAGTC TGCACTACAA TTATAACTGT
28701 TTTTGTATAT TGGGTTATT TTTTCAGAAG TAGGCCAGTA GCTCTAACAG
28751 GAGCCTCTTT AGCCTGAATT CGTCCAAGTA GTGCACTGTG GCACTAGTTG
28801 TCCCTCGGGA CATGCTCCCC AATACGTAAC TCACTTCAG GTGCAACTG
28851 GACACTTACT GGTAGTCAGA AATAGTATT GCATGGAGCT TAAAATGAAC
28901 TTGATCTTCG TGAAAGATGA GTCTGCAGCT AAGAGACTTT ACTGTATATC
28951 ATAGTGTGTTT TTTTTGTTT GTTTTGTGTT TGTTTTGTG ACGGAGTCTC
29001 ACTCTTCAC CCAGGCTGGA GTGCAATGGC GAGATCTTGA CTCACTGCAA
29051 CCTCCGCCCC CTAGGTTCAA GCAATTCTTC TGTCACCC TCCTGAGTAG
29101 CTGGGATTAC AGGCGCTGC CACCGTACCC GGCTAGTTT TGTATTTTA
29151 GTAGACACAG GGTTTCACCA CCTTGCCAG GCTGGTCTTG AACTCCTGAC
29201 CTCGTGATCC ACCCTCCCTG GCCTCCAAA GTGCTGGGAT TACAGGCGTG
29251 AGCCACGGCG CCCAGCCTGT ATCATAGTTC TTATGCACAA AGACCCCTTA
29301 ATATTGTTTG TAAATTCTCC CCTATGCACA CGCTGACCTG TTCTTAATC
29351 TTCTTATCTG TCTAGGTTT GAGCAGGTAT GTTAAGAAGT TAGGGGATTT
29401 TGCTAAGCCG GAGAATATTG ACTTGGCCGT GCAGTGCCTG AATGAACCTA
29451 TAACCAATGC ACTGCACCAAC ATCCCAGATG TCATCACCTA CTTTCGAGA
29501 CTCAGAAACC AGAGTGTGTT TAAACTCTGT GCTATTCCAC AGGTAGGGAA
29551 CGGGGCTCT CTGGGTGGAT ACGGGGCTAA AGGGAGTGGG GTAGGAGTAA
29601 GGGTGGATTT TGCTGTGCTA TATTCAAGGA TATGATTCCCT TAAAAAGACG
29651 ATGACTCCAG TTTATTACCG TGGGAGTTTC ATAGCACCCG CCTTTGCTTC
29701 CAGCCCACAA ACTCAGCTCA GCCTTGAGGT TAAGCCTGCT CCTTTTCAGA
29751 ACCTTCCTTC CGGAGTTACT ATTTCTACA GCTATCCTAA ACTAGTTAGG
29801 TTCTTTCTC CACAGTTAAG TCAAGGTCTT TGCTTAGAT TTATGGGAG
29851 TGCTGGTAA AACCTGGGTG AAGCTGTTAT CATTAAAAAG TCTTCATCAA
29901 GCACCTAATT ACTGCTGTC TTTTCCTAGA CCCGGCATAA AAAGAACCTG
29951 GTCCGGTAGA CCTAGCCTCT CAGTATGCTA GGAACCTACA CTTTTAGTT
30001 GCCTTACCA AGTATTGCGAG ATACTACTGC AAATAAGTGA AGAAAGTAAC
30051 AGCATTAAAC TGATTTGGGA ACTTGGTTTG ATCTTGTCT AATGACCCAC
30101 TTCCAATGGT GGTTGAAAGT AAAATCTGTA TCGCCGTCTT ATGTTCCAT
30151 TTACCTAGAA ATACTTTACC TTTGAGCACA GAAAATTAAT CCCCTCTGG
30201 TTGTTCTCCC CCTGGCATTG GTTTTAAATA TATAATGATT ATGTTTGTG
30251 TAGGAAAAAT AGAAAACAA CTACAATAGA AAATTCTTC CATATATTAT
30301 TTTGAAATAC ATATTTCGA TCCGATAATC CATTGCTCTA GCATGGAAAA
30351 TGTGGATTT ACTTGTGTTT GCTTTTCCA AAAAAATGG AACTTTGTG
30401 GCTACATTAT AGAATTGTTT TAGACTGCTT AATTCTGTGT GTTGTGAGA
30451 AAGGGAGGAG TGGGGAAGGT AAAATCTTG ACATACTTTC TTCTGGGTA
30501 TTTTTCTTG AGCGATTCCA TCTTAGTTGA TTAGCAGTTA GCAATTGCC
30551 ATTCAACAGA AGGTTTTCTT ACCTTTTGT GATAATGATA GCTAACGACA
30601 TCATTTCTTC TTTTTCCCT CTCTTCTTGT TGTCTCTAGG TGATGGCCAT
30651 TGCCACTTTG GCTGCCTGTT ATAATAACCA GCAGGTGTT AAAGGGCAG
30701 TGAAGATTGCG GAAAGGGCAA GCAGTGCACCC TGATGATGGA TGCCACCAAT
30751 ATGCCAGCTG TCAAAGCCAT CATATATCAG TATATGGAAG AGGTGGGTTT
30801 TTATTTAACT ACTTGGATAA TTTGTAGCTA CTTTTATGAT TTAGTAATGT
30851 CACTGTTAA CCAGGTTGG ATATTAGATG ATCCTAACAA TTCACTATCC
30901 TGTGGCCTAA AGAGACAGGA ATTGATATCC TTATAAGGA AAAAAGTCTA
30951 TTACACAGGAG CCGAGCAGAT TGCTCACTGC TGTTAGTAC CCTGGTGAGA

FIGURE 2J

31001 GGAGATAAAAT GGAGCAAGGC TGTAGGTTGG AGCCCCCTCAG TAGAATCATA
31051 GATTTTGAGC TGCAAGATGA TGCAGGAGGC CAACCCAAGCT TCTTGTGCT
31101 GGTGAGGAAT GTGAGGTTGA AGCTTGTCTG TGCTGATGCA GTGCGTGATT
31151 GAGTGGATCT CTGGCTCCCG TCCATGTGTC CTGACACCCA GTCTGGTACT
31201 TTCATTATGC CACAGGCCCTC AATTGAAAAA TCACAGTAGG GAATTTAGGC
31251 CAAGGAAAGC CATCAAGTTG CAATTATTTC CAAATTTC TTTGGAAAAT
31301 TTCATTCAA ATACCAAAAC CATCCTATAA AAAGAAAACT TACCTTCTTA
31351 GGTCAAATCT CTAATATTG ACTAGGTTCA AAAAGTTTAT TTCTGGCAG
31401 GCACAGTAGC TTACTCTGCA AATCCAGCA CTTTGGGAGA CCAAGGTGGG
31451 AGGATCACTT GAGGCCAGGA ATTCAAGACC AGCCCGGGCG ACATAGCAAG
31501 ACCCCATTTC TACAAAAAAAT TAAAGGATTG TCATGGTGGT GCACGCCGT
31551 GGTCCCAGCT ACTCAGGAGG CTGAGGCAGG TGATCACAT GAGCCTGAGA
31601 GGTGAGGCT ACAGTAAGCT GTGTGATTTC ATCATTGCAC TCTAGCCTGG
31651 GTGATAGAGT GAGACTTTGT CTCAAAAAAA AAAAAGCTT AAAAAGCTT
31701 AGAGACCAGA AGTCTCTGTA ATCTCTAATA ATCTCTAGGC CCTAGAGCAG
31751 TGGTTGTAA ATGGAGGTGA TTTGCTCCCC TCCCCCCAGA GGACATTGGA
31801 CAATGTCTGG AGACATTTT GATTGCTCTA ACCGGCAGGA ATCAGGGTGT
31851 ACTGGCATCT GGTGAGTAGA GGCCCCAGGAT GATGCTGTGA TCCTCAGGTG
31901 TGATCCTGTT GAGAATGAAA CACTGTAGAC TTTATGAAAA CATACAAGAC
31951 CCTCATCATT TTTCTTTGCT CTGAGCTCCC TCCCCAGAGG TTACCTCTGT
32001 TCATGGTTTT GTGCATCCGT CTAGTCCCCC TGTACCGGT TTACAGGAAT
32051 ATGGTTTGCA ACAGTGTTTT CATCTAAATA GAATTATACA AAATAGCGAT
32101 TTCTGATTTT TCTTGATAT TGCACATTCT TCTTATACTT CCTCCCTACC
32151 TTTATCTGAC ACAGAAATGC TGTATGTCCA GAACCTCTAT CAGAGGCACC
32201 TATGGAAGTC TAAGGGAAGA CCACATCGCT TTTAAAACC CTAAAATTT
32251 GTAGTCACTA GATGAAAATA TTCAGGCCAGT GACCCAAAAA ATTGCTACCA
32301 ATGAGACTCT CCATTTGCC ATGTAGGCCAG AACTTACTTT GATCTATGTG
32351 CCTGGGTAG TGACCAAGTA GGTGGGTAGG AGTAATCTCA GGGAAACTTG
32401 AGGCCCCAGC CTCATGGCTA GGGTCATAAT TTGAACCCAG GTCTGTCTGA
32451 CATCAGAACAT CATGATGTTA ACCCCAAATTCA TAAGGGTTC AACTACCCTT
32501 TCTAAATGGA ATCCTGCTAT ATTAAGCACT ATTTATTCTAT TTTATATAAA
32551 CTAGAAACAT TTTATGTAGT AAGTAGTTGA GAGTGTGTTG GTTTGCAGT
32601 TTGATCACTA GTTTAGAAA CCAGTTTTA AACACTTTGT GGCCAATTCC
32651 ATTACTATAT TAAAATTCAAG ATTTATTGTTG TTTTCTCTTA ACTATTGGGA
32701 TTAAATCCTG GTTGTAAITC ATAGTTTGAG GCGCAGGGTG GGCAGTCTAC
32751 ATTTGGCTGA GCCCTGTTT TGTGAATAAA TGTATCAGA ACACAGCCAC
32801 ACCCATTGTC TTCTATGTCT TCTGTGGCTG CTTTGCAAT GTGACGGCCG
32851 AGTGAGGAG CTGCAACAGG CGATGACTTG TAAAGCTGAA AATATTTTT
32901 GGCCTTGAA TAAGAGGTG GCTGACTTCT GACTTGGGC ATCAGTTGTT
32951 CTGTTATCCC AGTAAAACCTC AAGGCATTAG GGGAGAAATG TTAATATCAA
33001 TACTTAAGTT GATTGATTT AGGGAAATCT TTGAAGATT CTAAGTCTTA
33051 AGCAGTAGAA CCTGTTAATG GTTTAGTTT CAGCAGTAAG GACATTTCAC
33101 AAGTAAAGTT TAAAATGAAA ACATTGTA TGAAGGCCACA AGTCGTCTGG
33151 CCTCTGCTG GTGTCCAGAT ATTAACACTG ATCCTTATTTC TCCTGCTGA
33201 CCAAGTCTGT CTTTGATAGT AAGAAAGGAA GAAACGTTGA CTCTGTCCGA
33251 TCTCTGGACT TAGTGTGTA GCGAGCATGC ACCTGGAAAGG GACTTGCCAG
33301 AGGACCTCT CATGCTTCTC CAGTGTCTAG TGGGGGCTTG GAGTGCAGCC
33351 CCAGGTCTTC ACGAGCAGTT GGCCACACTG CAGGGCCCTC ACCCCACTCT
33401 GGAGCAGCT CTGCTTCAAA CCAGCTGGA TGCTTGTCAAG CTGGGGAGAA
33451 GATCAACCTG CTATTTGGG ATAGAAATAA ATGCTCAGCC AAACGGCCAG
33501 AAACCCCCAT TCCCCTCTCT GCCAAGTGA ATTCTTGGC AGGGAGAAGC
33551 TTGTTCTGTG CTCTGCACAC TTCTGTGCG CTCTCTGTGGT TAAGTCAGAG
33601 AATCATCCGG CTCTTTGAGC CCCAGGTGCG TAGCTGCTCA AGGATGGTCC
33651 CCAGCCAGCA GCTGCCAGGA ATCACCTGGG AGCCCCATTAA GACATCCAGC
33701 CCCCCCCCCA ACCTATCGAA TCAGAATCTG CCTTTTTTTC CAAATGATG
33751 TTTTGCTTT AATGGAAGTT TAGATGTTCA TAGACAAGAG TTTAAATGA
33801 TGATCAAGCT GATTCCATAT TCGCAGTTGT AAGTAGAACT GCTGAGACGT
33851 GGAAGTACCA CATGGACTCA CAGAGGAGCT GCTGTATGTA GCACAGCATT
33901 GCACAAGAGC TTATTTCACT CTAGTAAACA TTATAGGAG CCTGTGTCAT
33951 TTAATCATCA AGCCTCGCAC TGTGGCTCAC ACCTGTAATC CCAAAACTT
34001 GGGAGGCTGA GGCAGGCAGA TCACTTGAGG TAAGGAGTTC GAGACCAGCC
34051 TGGCCAATAT GGAAAACCC TGTCTACT AAAAATACAA CATTAGCCA

FIGURE 2K

34101 GGTGTGGTGG TGCACACTTG TCATCCCAGC TATTCCGGAG CCTGAGACAT
34151 GAGCATCGCT TGAACTCGGG AGGTGGAGGT TGTAGTGAGC TGAGATGGCA
34201 CCACTGCACT CCAGCCTGGG CAACAGGGTG AAGGCCCTT CTCAAACCTCC
34251 TCAAGTATTT GGCTTCAACT TTATGCCGGG CATGTAGATG AAAAGTCGGC
34301 TATGACCTGT CCTTGACAAAG CAGATGTAAC TCCTTGATTG AGGCTAGTAG
34351 GTTTTAAGA CCTGAATAAT TGAGTTGCA GAAACCTACT GTGTGCCCTC
34401 AGGTAAATGG AGAGTGGGGT TTGGCTTAGC AACGAAGCAT CTAGAAGGTC
34451 TCTTGGCCT TACCGGCTCT GTTTTAGGTA AGTCCACGTC TGAGTACCA
34501 TGACTGCAGC TCTTCCAGTT GTGCTGTATGTTTATATGT TAGAAATGAT
34551 CATCAAAGGA CTCAAAAGTT TTGCCACTAA TTGTATTACC GGGGACTGTC
34601 ACAACCAAGA TTTCTCTTAA TTATTTCACC TTACTTATCT CCTGGAAGGG
34651 CATATTGAAG TGCTCTTGGA GTTCTCTAAA AGGGTTTTTG TTGGTTGTGT
34701 ATATTCACTT GGGTGCCAGC GATTGATTCC AAATAAGTAA ATCTTTTTTC
34751 CCAAAAGGAT GTAAAGATGGC TTATGTTAT AAGTACAACA GGCTAACAAA
34801 GTACAAGTAG ATGAGAAAGT AAAATGAAGA AATAAAAGTCA TAGGAGCCAC
34851 AGAATTAACC CAGGAATGAA TAAGTGTGTA GTTGGGTGCT GATGTTATCA
34901 TCCTTCTTGT GTACATTGTC TGTACAGTTG CTCTGAGAAG GTAAGTCTTA
34951 AATTTCAAA AGTGAAGATGT CACCGAGCAT GTGGGCTGAT GCCTCTAATC
35001 TCAGCACTTT GGGAGGCTGA GGCAGGCGGA TCACTTGAGG TCAGGAGTTC
35051 GAAACCAGCC TGACTTATGT GATGAAACCC TGCTCTACT AAAAAAAA
35101 AAAAAAAA AAAAAAAA AAAAATCCAA AAGTTAGTTG GGCATGGTGG
35151 CAGGTGCTG TAATCCCAGC TACTTGGGAG GCTGAGGCAG GAGAATCGCA
35201 TGAAACCTGGG AAGTGGAGGC TGCACTGAGC CAAGATTGCA CCACTGCACT
35251 CTAGCCTGGG TGACAGAGCG AGACACCATC TTAACACAC AAAAAAATCT
35301 ACAATATACC AAAACCAATTA CTTACCTGAG AAACATTCT CAGGGTCATT
35351 GTAGTGAATG CCTATTATGAT GGCTTTGAT GGCAATCAGGG CACTCAGGTC
35401 ATTTACAAGA GTAGTGTGTG AGACCTCTGT TGTCACTGCC ACTCATCTG
35451 GCCTTCGGCC ACTGCTGTAG CAACCAGTTT CCAAGTAGGG CTGGACCTTG
35501 CCTCTGCTC CAGAGACCTC TCGCTCCCTG CCCTTGGGCT TCTGACGAGC
35551 TGCAAGAACT GCCTGGCACG TGGGTCCCCA CAACCCAGAG GAGGTGAGGG
35601 CCACCTCTCT GCTCTCAGG GCCACCTTTC ATAAGGCTCC TTGAAGGTCC
35651 CTCAAGATCA AGCCAACCTCA ACACATCCTT GATAGGCCTT CCTGCCTTCT
35701 GTTCACTTC TCCACTCGTT TCCAATAAA TGGCTGCATG CAAGCTTTG
35751 CCTCAGGTTG TGCTTTTAGG AGGAAGGCTA AGACAAAGCAG TAAAGCAACA
35801 TGGGCAGGCA GAAGGATGAC TTCTAATAGA ATTATCTCAT CACTATATAT
35851 TTTACTTTAT GGATGCTTGT ATTGAAAAGT CTGGCTGGG TGGAGTGGCT
35901 CACGCCGTGA ATCCCAGCCC TTTGGGAGGC CGAGGGGGT GGATCACTTG
35951 AGGTCTGGAG TTTGAGACCA GCCTGACCAA CACTGGTAAA ACCTTGTCTC
36001 TATTAACAAAT GCAAAATTA GCCAGGGATG CACGCTTGCT GTGTGCCAGC
36051 ACAGGGCTAG GCTGGAGATA AAAAGGTGAG TAAGTAGGTG CGGTGTAGTC
36101 AGGGTGAAAAA CTACAGATGG TCCATTCCA CGTAAGTGGA AAGGTAAGG
36151 TATGTACAAT AGGGTGGCTC CTGGCTGAAC CTGGAGCTGC AGACAGGTTT
36201 TCTAGAAGGC ATAATCCTGA AGITGAGACT TGGGGGCCCTA GGTAGGAGCC
36251 AGTTGAAGGG ACGTGGGAGG CGCATTCCAG AGAGAAGGGAG TGGTATGAGA
36301 CTGGAACAGA GGTGTGAGC AGCATCGCAT GGGCGAAACA ACAGTAGACA
36351 GTTGTCTT TGTTTTGTT TGTTTTTGA GACAGGGTCT TGTTCTGTCA
36401 TCCAGGCTGG AGTGCAGTGG CATGATCTCG GATCACTGCA ACCTCCACCT
36451 CCCAGGCTCA AGTGATCTTC CCACCCAGT CCCCAAGTAG CTGGGGGACC
36501 ACAGGTGCAT GCCACGATGC CCGGCTAATT TTGTACATT TTGTAGAAC
36551 AGGGTTTAC TGTGTGTCC AGGCTGGTCT TAAACGCCTG AGCTTAAGCA
36601 GTCTACATGC CTCAGCCTCC TGAAGTGTG GGATTCCAAA CATGAGCCAC
36651 TGTGCCCTGG CCGGCAACTG TTACTAGACT ATAGAGAGGG AGGTGGGCAA
36701 GGGCTGGTGA CACTAGACAG GTGCAGTAGG TCTGGACCAT GGGTGGCCTT
36751 GCGCTACACA TTACAGAGCT CAGGCTTTT TTCTCCAGGT GAGAGGGCTG
36801 GTGCCACTGA GGCATCAAGC AGAGGTTGAG GATCTCCTTG GTGACAGTGT
36851 AGAGCAGACA GGTAGATTG GGAATTAAAG CTTAGACTCA CGTTGGAGAC
36901 TGAGATAGCT CATCTGAGAG GCACTCAGGG CCTAATCTCA GGCAGTAATT
36951 TTAGGGATGT AGGGGAAGAG ATGGATTCTG CACATACTTG GGAGGCTGT
37001 GGAGGGAGTG GGAGGGAGGC ACAGGGAGGA CTCCAGGGTG GTTCATACGG
37051 CTCCCTGCTT CTGTTCTGT CCCCTTTGT CAAGCTGTGG TCTGTACTGC
37101 GTGTTCCATC TTGTTCTAA GCTGCTTTG CCCAGTCTTT CCAGCATTC
37151 CTTTCGTCA TGTTAGTCTG TGCCTGTCTA CGTGAACATAT GGTGACGTTT

FIGURE 2L

37201 ATTGGGCCTG GCACTGTGAG GTGCTGGGA TGTGAAGATC ATTGTGGCTC
37251 AGCCGCTGCT CTCGAGGGCC TCTGGGTGCA GTATGCACAC CTGTGCCTCC
37301 TGTGGCTCA GGAAGACAGG CTTTGAGATG AGCTGGGCT GACATCCCCA
37351 CCTTATCATT GGGATGGCTT TGGGTAAGTT ATGTTCATGT TCTCTGAGCC
37401 TCCCTTCCT CATTGGTAAA ATGGGTATAA AATACCTGCC AGTGGAGGGT
37451 TGTGTAAGT AGCCATGGAA AATGTAAGC ACATAGCACT TACCATTTC
37501 TCCTGTGCT TTAACAGATT TATCATAGAA TCCCCGACTC AGACCCATCT
37551 TCTAGAAAA CAAGGCAGAT CATCTCCACC ATCCGGACGC AGAATCTCC
37601 CAACTGTCAG CTGATTTCCC GAAGCCACTA CTCCCCCATC TACCTGTCGT
37651 TTGTCATGCT TTTGGCTGCC CTGAGCTGGC AGTACCTGAC CACTCTCC
37701 CAGGTAACAG AAGACTATGT TCAGACTGGA GAACACTGAT CCCAAATTG
37751 TCCATAGCTG AAGTCCACCA TAAAGTGGAT TTACTTTTTT TCTTTAAGGA
37801 TGGATGTTGT GTTCTCTTTA TTTTTTCCCT ACTACTTTAA TCCCTAAAAG
37851 AACGCTGTG GGCTGGGACCC TTTAGGAAAG TGAATGCAG GTGAGAAGAA
37901 CCTAAACATG AAAGGAAAGG GTGCCTCATC CCAGCAACCT GTCCCTGTGG
37951 GTGATGATCA CTGTGCTGCT TGTGGCTCAT GGCGAGAGCAT TCAGTGCCAC
38001 GGTTAGGTG AAGTCGCTGC ATATGTGACT GTCATGAGAT CCTACTTAGT
38051 ATGACCTGG CTAGAATGAT AATTAAAAGT ATTAATTG AAGCACCATT
38101 TGAATGTTCG TACTAGTAGA AAATGATGTG AATTTCCTTT CTGTCGGCT
38151 CCTATTTTC TCATCATTTT GTTTCTTTA ATTGGGTTGA ATGGAGTAGA
38201 TAGAAATATT TATGGTTAG GTAACAGTTA GATGTTCCCT AAGAATGCAA
38251 ACTGCCTTTT CCACACAAAG GCTGGGAATA AAATTCTGGG TATTCTCGTA
38301 TTCTCATTTA AAGGAGTTA GCTTCAGAG AGAAACAGCA GGATTGCTTT
38351 TGACCTTTA GAAGATTGGT CTCCAGTAA GGTGGACATT TTTGAGATTT
38401 TTATAATAAA GAATTTAATT GCTCTGCATT TGTCAAGTAC AGTTCGCTTG
38451 AAAGCCTGCC TGACTGTGGA AAAGATGGAG CTCAGAAATG GAGTTGATGG
38501 CCCAGCGTGG TGGCTCATGC CTGTAATCCC AGCACTTGG GAGGCTGAGG
38551 CGGTCGGATC ACGACATTAG GGGATCGAGA CCATCCTGGC TAACACGGTG
38601 AAACCCCCGT CTCTACTAAA AAAAAAAAATTAGCCAGG CGTGGTGGCG
38651 GGTGCTGTGTTCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCTTA
38701 AACCCGGGAG GCGGAGCTT CAGTGAGCTC AGATCGCGCC ACTGCACTAC
38751 CAGTCTGGGC AACAGAGCGA GACTCCATCT CAAAAAAAGG AAAAAAATTGT
38801 AAAAAAAA AAAAAAAAAN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
38851 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
38901 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
38951 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39001 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39051 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39101 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39151 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39201 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39251 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39301 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39351 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39401 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39451 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39501 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39551 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39601 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39651 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39701 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39751 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39801 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39851 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39901 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
39951 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
40001 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN
40051 NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN (SEQ ID NO:3)

FEATURES:

Start: 2058

FIGURE 2M

Exon: 2058-2156
 Intron: 2157-7996
 Exon: 7997-8094
 Intron: 8095-8869
 Exon: 8870-9053
 Intron: 9054-25147
 Exon: 25148-25339
 Intron: 25340-29365
 Exon: 29366-29542
 Intron: 29543-30639
 Exon: 30640-30792
 Intron: 30793-37517
 Exon: 37518-37736
 Stop: 37737

CHROMOSOME MAP POSITION:
 Chromosome # 8

ALLELIC VARIANTS (SNPs):

Position	DNA Major	DNA Minor	Domain	Protein Position	Major	Minor
825	G	A	Beyond ORF(5')			
2632	C	T	Intron			
4430	C	T	Intron			
4791	C	T	Intron			
4886	G	C	Intron			
4887	A	T	Intron			
4889	T	A	Intron			
5110	G	T	Intron			
6911	G	A	Intron			
7212	A	G	Intron			
7355	C	T	Intron			
7398	T	C	Intron			
7653	T	C	Intron			
8310	A	G	Intron			
8145	C	T	Intron			
8031	G	A	Exon	45	R	K
8462	G	C	Intron			
8873	C	T	Exon	67	N	N
9190	C	T	Intron			
9311	T	-	Intron			
9847	T	C	Intron			
10460	C	T	Intron			
20204	G	A	Intron			
20362	C	A	Intron			
21166	G	A	Intron			
21477	G	A	Intron			
22230	C	T	Intron			
22941	A	G	Intron			
23963	C	T	Intron			
25686	A	C	Intron			
26018	A	G	Intron			
26078	G	A	Intron			
26625	C	G	Intron			
27151	C	T	Intron			
28032	G	A	Intron			
28772	G	A	Intron			
29572	C	T	Intron			
29761	C	T	Intron			
30732	G	C	Exon	281	L	L

FIGURE 2N

30841	G	T	Intron
31376	G	A	Intron
32032	A	G	Intron
32525	A	G	Intron
34179	G	T	Intron
34249	T	C	Intron
34451	T	C	Intron
34532	T	C	Intron
36541	T	C	Intron
36607	A	G	Intron
36681	A	G	Intron
37493	C	T	Intron
37966	C	A	Beyond ORF(3')
37973	T	C	Beyond ORF(3')
38113	C	A	Beyond ORF(3')
38298	G	C	Beyond ORF(3')

Context:

DNA Position	
825	<pre>GCAGTGAACTGACAGGTTCTGTTGAGATGAAGTCTCGCTTGTCC CCCAGGCTGGAGTGCAATAGCGGATCTCAGCTCACTGCAACCTCTGCCTCTGTGTTCA AGCGATTCTCCTGCCTCAGCCTCCAGGTAGCTGGGATTATAGGCGCTGCCACCATGCC TGGCTAATTTTGTTAGTAGAGACGCAGTTCAGCATGTTGGCCAGGCTGGTCTT GAACCTCCAGACCTCAGGTGATCCGCCCTGGCTCCAAAGTGTGCTGGGATTACAGGC [G, A] TGAGGCCACCGCGCTCGGCTAGACCTGACAGGTTAAAAGGATTACTGGTGCTGTGTTA AAACAGACTGCAGGATGGCTTAGGTAGCCAGTAGGTTTTTTGGAGACGTAGT CTTGCTCTGGCTGGCTGGAGTGCAGCGTGTACTCTGGCTACTGCAAACCTCCGC TTCGGGTTCAAGTGTATTCTCCTGCCTCAGCCTCCGGAGTAGTGGGACTACAGGC CACCACACACTCGGTTTTTGTTAGTAGAGACGGGTTTACCATGTTGGCCAG</pre>
2632	<pre>GCCGTCTGGCTGACCTGTCCTGCCCTGCCCGCAAGCCGCCCTGGCATGAGCGACTTTGC GTGGTCCCGTGGTGCCTCCCGTTCTGCTCCCTCCGTGAGCATGGCGCTTACCGG TATTTAACCCGAGGGTACACATCTGAGGCAATGTGGGGTTACGGGGAGAGGACG AGTGAGTTTTTGTTAGCGGAATGAACTATGCAGATAACATCACATGAAGCCGTTCT GGAATGAAGTCTGACTCCCTCAGTTCACACCTCTCCGGAGCTCCCGCCTGCTG [C, T] CTTCCATCGCTTCATCCTCGGTGCTTCCTGAGTTAAAATCGCTATCTACGCTTCAA GTTCCAATGAGTTATCTAACGCTATGGATTAGCTAGGTGGTGGAGGTCAAGAACT TGGTTTACTTAGATTTTATCTGCTCATGCCGTACTATTGTTAATGAATGCATAG GAGGTGTTTATTCCAACAAGAAAATTATTCTGACCGATTATTGAATGAATAGACAAA TTCAGCCAAGTCTCTGGTCTGGACCGCCGGCTGATTCTGTAACTTTTGGGCCA</pre>
4430	<pre>GGCTTTTTTTTTTTTTGAGGGGGGGTCTCACTCCATCGTCCAGGCTAGAATGCT GTGGCCTGACATGACTCACTCCAGTTTGACTCCTGGCTGAAGCCATCCTCCACCT CGGCTTCCGTATCCGAGTAGCTGGACTCCAGGCACGTGTCACCAATGCATGGCTAATT TTAAATTGGTAGACACAATGTCTCGCTGCATTGCCAGGCTGGCTTGAACCTCCT GAGCTCAAGCGATTTCCCACCTCAGCCTCAAAGTGTGGGATTACAGGTGTAGCCAC [C, T] GCACCCAACCAGTTCTCTGCAAACCTAGGGAAAAAATTACGCTTAGCAGATATTGAG GGCTGATTATTCTATCACAGAACGATTGGCTATAGAATTTCAGGGTTAGTAAACTTG ATTTACACTGAATTGGTAGGTGCATATCAGTAATCTACGGGCTATGCCGCTGCAAGT TGTGTGGCATCACCAAAAGCCGAGAGTAATGGAAAGAGCAGGCTGTAGTAATCAGGCA GATCTGGCCTCTGTCCAATCTAAATCCTGTTATTAGACTAATATCTTAAGTCTGTTATT</pre>
4791	<pre>GGCTGATTATTCTATCACAGAACGATTGGCTATAGAATTTCAGGGTTAGTAAACTTG ATTTACACTGAATTGGTAGGTGCATATCAGTAATCTACGGGCTATGCCGCTGCAAGT TGTGTGGCATCACCAAAAGCCGAGAGTAATGGAAAGAGCAGGCTGTAGTAATCAGGCA GATCTGGCCTCTGTCCAATCTAAATCCTGTTATTAGACTAATATCTTAAGTCTGTTATT AGTCCGATTCTGACGCTATTAAGTTAGGTGAACAACCTGGTAACCTAACCTCTGAAC</pre>

FIGURE 20

[C, T]
 ACAGTTACTCATCTGAAAATAGGGATGTATGTATGGTAACGATTTTAACCACAACT
 TCCCACTCTAAGATGGTCTGAAAAGAATTGGTGGCTCAGAACACTGGC
 AGCAAAACCTGACTTGAAGTTGAGGCTTCATTCACTCCACTAGTATATTCAAATGTTT
 GCTAAAGAAATAATTATGAGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTAT
 TGCCTATTTCTAAAACACTAAAATGCTAAATTCTGCCAGGTCTGCCACAGATGTT

4886 CTACGGGCATATGCCGCCTGCAAGTTGTGGCATCACCCAAAAGCCGAGAGTAATGGAA
 AGAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCATCTAAATCCTGTTATTT
 AGACTAAATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAAC
 AACCTTGGTAACTTAAACCTCTGAACCACAGTTACTTCATCTGAAAATAGGGATGTATGT
 ATGGTAACGATTTTAACCACAACTTCCAACTCTAAAGATGGTCTGAAAAGAATTTTT
 [G, C]
 AGTGGTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCA
 CCCACTTAGTATATTCAAATGTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACT
 GACTAGGGTTGTATATGCATTTATTGCTTAAACACTAAAGCTAAATTGCTAAATT
 TGCCCCAGGTCTTGCACAGATGTTCACTGGACTATGGGCTGTGAGACCTTAAAGGGT
 TGATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG

4887 TACGGGCATATGCCGCCTGCAAGTTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAA
 GAGCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCATCTAAATCCTGTTATTTA
 GACTAAATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACA
 ACCTTGGTAACTTAAACCTCTGAACCACAGTTACTTCATCTGAAAATAGGGATGTATGT
 TGGTAACGATTTTTAACCAACACTTCCAACTCTAAAGATGGTCTGAAAAGAATTTTG
 [A, T]
 GTGGTTGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCA
 CCACTTAGTATATTCAAATGTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTG
 ACTAGGGTTGTATATGCATTTATTGCTTAAACACTAAAGCTAAATTGCTAAATTCT
 GCCCCAGGTCTTGCACAGATGTTCACTGGACTATGGGCTGTGAGACCTTAAAGGGT
 GATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTG

4889 CGGGCATATGCCGCCTGCAAGTTGTGGCATCACCCAAAAGCCGAGAGTAATGGAAAGA
 GCAGGCTGTTAGTAATCAGGCAGATCTGGCTCCTGTCATCTAAATCCTGTTATTTAGA
 CTAATATCTTAAGTCTGTTATTAAAGTCCGATTTCTGACGCTATTAAGTTAGGTGAACAC
 CTTGGTAACTTAAACCTCTGAACCACAGTTACTTCATCTGAAAATAGGGATGTATGT
 GTAACGATTTTTAACCAACACTTCCAACTCTAAAGATGGTCTGAAAAGAATTTTGAG
 [T, A]
 GTGGGGCTCAGAATCACTTGGCAGCAAAACCTGACTTGAAGTTGAGGCTTCATTCA
 ACTTAGTATATTCAAATGTTTGCTAAAGAAATAATTATGAGGTGCTACTTCACACTGAC
 TAGGGTTGTATATGCATTTATTGCTTAAACACTAAAGCTAAATTCTGC
 CCCAGGTCTTGCACAGATGTTCACTGGACTATGGGCTGTGAGACCTTAAAGGGTGA
 TTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCATGGAGTTAAGTGCTTGATA

5110 AAATAGGGATGTATGTATGGTAACGATTTTAACCACAACTTCCAACTCTAAAGATGGT
 CTGAAAAGAATTTTGAGTGTGGCTCAGAACACTTGGCAGCAAAACCTGACTTGAA
 GTTGAGGCTTCATTCACTCCACTAGTATATTCAAATGTTTGCTAAAGAAATAATTATG
 AGGTGCTACTTCACACTGACTAGGGTTGTATATGCATTTATTGCTTAAACACTAAAC
 CTAAAATGCTAAATTCTGCCAGGTCTGCCACAGATGTTCACTGGACTATGGGCT
 [G, T]
 TGAGACCTTAAAGGGTTATTGAGTAAGGATCACAGGTGATGTCCGCATTGTGCTTGGCA
 TGGAGTTAAGTGTGTTGATAATGGTGGTTATCAATCTGATTATGAAATTGTAATT
 CAGTTCTCAAGTTGTGGTTTTTCCCTCTGGAGAAATCTATTCTATTAAAGTGA
 GGAAGGCTCCGTGGAGGGCTGGTAGCTGGTAGCTGTTCACTGTGGAACCTTCAGCCTGA
 GGCTGGAGCCCCCTCCTGGAGTCTGGTCTTGTGCTTCCGACCAACCCCCACACCCCTT

6911 CCACCTTGGCCTTCCGAAGTGCAGGGATTATAGGCCTGCGCCACTGCACCCGGCCCTGTT
 GGATAAAATGATTCCAGTCTCTCCAAAAGAACACTGTTGTAAGACTGTGGGTGAGGGGAG
 GGAAGGGACAAATAGGAACCGCCGTATTTCCACTCCCTGTGGGCTAAAACCTGCTCTA
 AAAAATAGTCCATGAAAAAAACATAGTACAAACAGCAACTCTTCTGATATGCTTGAT
 TTAAAATCAGGTTTTCTCCCTTGGAAAAACACAGTCCTGTTGCTTTAGGAAAGA
 [G, A]
 TAAAGGTCACTGCGCTGCATTGCTTAATTCAAGGGAAAGATGAGAAGACATCTGAA

FIGURE 2P

AGGAATGGCTGGCTTCTAGAGAATAGTAGAGGCTTAATAGGTGTATAGAAAAACCAGG
 GTTGGACAGTGGTAGTAAACGGAAAACAGATTTATTACAGAAAAACTACTGCAGTAAG
 AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA
 TGGCGGGGGAGCCGGATGTCAGTGGATGAAAATTATTACGAGGAAACACAGGGGTGTGC
 [A, G]

7212 TAAAGGTCACTGCGCTGCATTAAATTCAAGGGAAAGATGAGAAGACATCTGAA
 AGGAATGGCTGGCTTCTAGAGAATAGTAGAGGCTTAATAGGTGTATAGAAAAACCAGG
 GTTGGACAGTGGTAGTAAACGGAAAACAGATTTATTACAGAAAAACTACTGCAGTAAG
 AGGAGAGAGACCTCGGTACAGAACTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGA
 TGGCGGGGGAGCCGGATGTCAGTGGATGAAAATTATTACGAGGAAACACAGGGGTGTGC
 [A, G]
 TTCTTGCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGATGTGG
 AACCTAATCGGCTGTCAGGGTGTACAGATACTGAAGTTGGGGATTCTGGTCAAATCAA
 TTAGCAGGATTCTGGTAAAACGGCGATGCAAAGACAGATGGCTTGAGTACAAAGTC
 CAGGCTTATTGGGAAAGAGGATTTCAGCGGAGCCGAGTAGAGTTGGTCTAGGGAGACT
 CTGTCACTGGGAGGACGAGCAGGCCGCTCGGAAGTGCCTGGGTTCTTAGCGGCCAGT
 [C, T]

7355 CAAAACAGATTTATTCAAGAAAACACTGCACTGAAGAGGAGAGAGACCTCGGTACAGAA
 CTGCTCCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCGGGGAGCCGGATGTCAGT
 GGATGGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTGCTGAAGGCAGGCCAGA
 GTTATCAGACATCACCTGAGGGATGGAGGGGATGTGGAACCTAATCGGCTGTCTAGGGT
 GATCAGATACTGAAGTTGGGGATTCTGGTCAAATCAATTAGCAGGATTCTGGTAAAA
 TGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGGCTTATTGGGAAGAGGATT
 TCAGCGGAGCCCGAGTAGAGTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGCGAG
 CCGCTCGGAAGTGCCTGGGTTCTTAGCGGCCAGTGGGTTCTGGTGAGAAGGGCAACA
 GCGGGAGGAGGCGCCGCTGCGGAGCGGGAGGGCGGGGGCTGCGGGCTGCGGG
 GGGCCCGTTGTGGGTCGGCCAGCGCGTATTGAGTAGAGGGCGAGCCGTCGGCCTCT
 [T, C]

7398 GAGACCTCGGTACAGAACTGCTCACTGCGAATACAAAGAAAAGTAGGAATTGATGGCG
 GGGAGCCGGATGTCAGTGGATGAAAATTATTACGAGGAAACACAGGGGTGTGCATTCTT
 GCTGAAGGCAGGCCAGAGTTATCAGACATCACCTGAGGGATGGAGGGGATGTGGAACCT
 AATCGGCTGTCTAGGGTGTACAGATACTGAAGTTGGGGATTCTGGTCAAATCAATTAG
 CAGGATTCTGGTAAAACGGCGATGCAAAGACAGATGCGTTGAGTACAAAGTCCAGG
 [T, C]
 TTATTGGGAAGAGGATTTCAGCGGAGCCCGAGTAGAGTTGGTCTAGGGAGACTCTGTC
 CTGGGAGGACGAGCGAGCGCTCGGAAGTGCCTGGGTTCTTAGCGGCCAGTGGGTT
 TGGTGAGAAGGGCAACAGCGGGAGGAGGCGCCGGTGCAGCGGGAGGCGGGGGCGGG
 CTGCGGGGCTGCGGGCGGGCCCTGTGGGTCGGCCAGCGCGTATTGAGTAGAGGGC
 GAGCCCGTCCCGCCTCTGCGGCGCTTCCAGATCTGCTTGAGTATGGAGGAAAAAA
 [T, C]

7653 AACTGGCGATGCAAAGACAGATGCGTTGAGTAGACAAAGTCCAGGCTTATTGGGAAGAGG
 ATTTCAGCGGAGCCCGAGTAGAGTTGGTCTAGGGAGACTCTGTCACTGGGAGGACGAGC
 GAGCGGAGGAGGCGCCGGTGCAGCGGGAGGCGGGGGCTGCGGGCTGCGGG
 GCGGGCCCGTTGTGGGTCGGCCAGCGCGTATTGAGTAGAGGGCGAGCCGTCGG
 [T, C]
 CTCGTCGGCGCTTCCAGATCTGCTTGAGTCTATGGAGGAAAACCCGCGGGTCCGC
 GATTCCCATGGCGCAGCGCCTCGGGCAGGGCCATGGCCCTCTCAAGCGCACCTT
 GGTGCTGAGTCCCGCCGCGCCAGGGCCGGCGCAGGCACCGCCCCGCGGGCTG
 CTGCTTGCCTCTGCGCCTGGCCCTGCAAGGACTGGCCTCGGGAGAGGGCGCAGGCT
 GTGGAGCCGCTGCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCCAGTCCC
 [A, G]

8310 CAGCCTGAAAACCTGCTACAAGTATCTCAATCAGACCAGTCGCACTGGCTGTGTT
 CCAGGGCGCTGGATGGGAAATGCGGTGAGTAGTGATGGAGGAGCAGCGCCTCTGGCTTGAGGAA
 AGCTGTCCGGACTTTGAGTGTGTTGAGTAGTGATGGAGGAGCTACCTTTGATATAGCGCTCAGCGTTG
 CAGCCTCGTTGCTGGCTTATCCAGAACATAGCCGGCCCTACGTGTTACTTTAGAAA
 GCGCTTCCAGGCTTTGCCATCTAGTAGAGTCCCTGCGGGCCAGCCTTCAGAGAAG
 [A, G]
 GGGGGAGGGGGTGTGTTATTAACTTTTTAGTCTTGGCAGCTGAACCTGCGCTGTGA
 GCAGGTGGTGTATTCTCGGCTTCCCTATCCAACCTTGCAATTCTAGCATATT
 GGGTTGATTCTTTGAAGCTGCCTCTGTCACATTACACCCATGAACCTAGACCAGTTGC

FIGURE 2Q

CTTTATGTATGATCGTATTTACTGAGAAGTTACTGTGTTTTGACTTCTTTCTAT
 TTGCTACATATTAGTCGGTCTAACGTTGGCTTCTGGCTCCATAGTCTACATTG

8145 CAGCCTGAAAACCTGCTACAAGTATCTCAATCAGACCAGTCGCAGTTCGCAGCTGTTAT
 CCAGGCCTGGATGGGAAATCGGGTGAATGGAGGCAGCGCCTCTGGCTGGAGGAA
 AGCTTGCCGGAC
 [C, T]
 TTTGAGTGTGTTGGAAGCTACCTTTGATATAGCGCTCAGCGTTGCAGCCTCGTGTGT
 GGCTTATCCAGAACATAGCCCGCCCTACGTGTTACTTAGAAAGCCCTCCAGGCTCT
 TTGCCATCTAGTAG

8031 CAGCCTGAAAACCTGCTACA
 [G, A]
 GTATCTCAATCAGACCAGTC

8462 GCTACCTTTGATATAGCGCTCAGCGTTGCAGCCTCGTGTGGCTTATCCAGAACAT
 AGCCCGCCCTACGTGTTACTTTAGAAAGCCCTCCAGGCTCTTGCATCTAGTAGAG
 TCCCTGGGGCCACGCTTCAAGAGAAGGGGGGGAGGGGTGATGTTATTAAACCTTT
 TTAGCTGGCAGCTAACCTGCCTGTGAGCAGGTCGTGATTCTGGCTCCCTATC
 CAACATTGCATTCTATTCTAGCATATTGGTTGATTCTTGAAGCTGCCCTGTGCA
 [G, C]
 ATTACACCCATGAACCTAGACCAGTTGCCTTATGTATGATCGTATTAACTGAGAAGT
 TACTGTGTTTTGACTTTCTTTCTATTGCTACATATTAGTCGGTCTAACGTTGG
 TCTTCTGGCTCCATAGTTCTACATTGGTTAAATGCAACTCACTCTGGAGTAGTGGT
 ACATTCAACTAGTAGGCTTTAAATAAAACTACAGAAGTTCATTACTCTCATGTAAGGAAG
 GAAAACATAATGTAACCTTCGTTAAGTATGAAAGCGTTGGATATCCTTATAGTCCTT
 8873 AAACGTTGGCTTCTGGCTCCATAGTTACATTGGTTAAATGCAACTCACTCTGGG
 AGTAGTGGTACATTCAACTAGTAGGCTTTAAATAAAACTACAGAAGTTCATTACTCTCA
 TGTAAGGAAGGAAAACATAATGTAACCTTCGTTAAGTATGAAAGCGTTGGATATCCTT
 AGTTCTTAGAGTTAAGGGTGAGATGGGTTAGAAAGTGGCCAGGCACAAGTTATTAA
 AATAAAAAATCTTGGCTGTTGTTCAATATATTAAAGTTCCTTACAGCAA
 [C, T]
 GCAGTGTGCATATTATCTGGTCTCCGAGCTCTGGACACACTGGAAAGATGACATGACC
 ATCACTGTGAAAAGAGGTCCCCTGTTACACAACCTTCACTCTTCCCTTACCAACCA
 GACTGGGGTTACGCATCTGCTACGGACTGTTGTCATAATTGCTAACGGTGGGACTTCC
 GTGAGTGGGGTACGCTTACGGACTGTTGTCATAATTGCTAACGTGGT
 TCCGGTAGCCTCCACATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGT
 GAGGGTTAAAAACTC

9190 ATCTGGTTCTCCGAGCTCTGGACACACTGGAAAGATGACATGACCATCAGTGTGGAAAAGA
 AGGTCCCCTGTTACACAACCTTCACTCTTCCCTTACCAACCGAGACTGGCGGTTACGG
 AGAGCAAGGAGAAGGATGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGC
 ATCTGCTACGGACTGTTGTCATAATTGCTAACGGTGGTGTCCGGTAGCCTCCATA
 CATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTTAAAAACTC
 [C, T]
 GGTAGCCAAGACTCTGAAGCCAGGCTGCCCTGGGTTGGAACTCTCAAATCTCCCACTTACTA
 AACTGTGGTTACTTACAAAGACTCTCTGTGCCCTCAGTTCTTCATCTGAAAATAGGG
 TAATAATAACACCTACCTCATGGTATTCTGAGGGATTCAAAGAATTACGTAGGTAATGCT
 CTTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAAGTCCAGTGGTCTTCTCTGTG
 GGAAGACGCAGTCATAATTAGTGTGAAAGATTCTCAGGCTAGCTCACAAAGCCTG

9311 GAGCAAGGAGAAGGATGCCAGGTGCTGGAGGACTTCCCAACGGTGAGTGGGGTTACGCA
 TCTTGTCTACGGACTGTTGTCATAATTGCTAACGTGGTGTCCGGTAGCCTCCATAC
 ATGTGGAGAAAGGTTAAATAAGCATTCTGAGGGCAGCATAATGTGAGGGTTAAAACCTC
 GGTAGCCAAGACTCTGAAGCCAGGCTGCCCTGGGTTGGAACTCTCAAATCTCCCACTTACTA
 AACTGTGGTTACTTACAAAGACTCTCTGTGCCCTCAGTTCTTCATCTGAAAATAGGG
 [T, -]
 AATAATAACACCTACCTCATGGTATTCTGAGGGATTCAAAGAATTACGTAGGTAATGCTC
 TTAGAATGTTAGCTACTGCTGTTATTATCAGTATTGGAAAGTCCAGTGGTCTTCTCTGTG
 GAAGACGCAGTCATAATTAGTGTGAAAGATTCTCAGGCTAGCTCACAAAGCCTGC
 CGACTGTATGATGCAGCCTACCTGTAACACTGCTGCCCTTGACTACCCGGAGCCTGGT
 AGCATGGGACTGCTGCTCACGATGGCAGCAGCCTGGCATGGGGCGGTGCTGTTGGCA

FIGURE 2R

9847 CTGGTAGCATGGGACTGCTCACGATGGCAGCAGCCTGGCATGGGGCGGTGCTGT
 TGGCAGCTAGGGCAGCCTGCACTTCACCTGTATCTGGCAAGTCTTATCTGC
 TTTGTGTCCTCGTCTCTCGTTAAAGTTAGAGCTGAGAGGATTAATTCGCACATAT
 AAAGTACTTAGTGCTGGTACAGGGTAAGTATTCTGTAAGTATTAGCTATTGGTCTATT
 TTGGTAGGAAAGTGGTTATAGTTAAACCTAAGATTAAAGTCCCTCAAGTTCA
 [T, C]
 GTGGACATCTGCCTAGGCCTACTATCCTAGAATTGCATGCTTATCACACAAATAACT
 GATTCTCCATATCTTATAAAAGGTTGATTAGCAAAGTCACATGTTGTAATAG
 CTGAAAGAAGCCCTTTGTCACAGTTGCCAGAGCTTGGAGAACAGTCCTATGTTA
 TTGAAACAAACCTAATCTGAGCTGAGTTGGAGGGAGCTAAGTGGACAGAGAGTCCTCC
 ACCCAAACAAAAGAATCTTGATCTGGCATAATGGGAGCAATATTAAAAAAAAAA

 10460 AGGAATGTTGGGAAGACTCTGGGTGCAAAGGCTGTTGAGATTGCTGAGATCAGAC
 CTTAAGTACCAAAGCCAAATATAGTACAACATAATACAATGAGAAGAAAATAGCTGAA
 GAATAATTGAGTTTATAACAGTACAATTCAAGAGAAGAAAATTATGACGACTAGC
 TGGTGAGAATTAGAACTGTAACCTGGGAAGGTCTGGTGATTGACTCTCACAGGG
 CCTGATGACCAGAGGATGGGTTCTTGATGGAAATCTGTCGATTGATGGC
 [C, T]
 TCTGAATTCTGCTGAAGCAGAGGAAGTAGTAATACCCATTATAATGGAAGTGCATTCT
 CACTTAAACAACTAATATTATTCTAGCTGACCTAGCCTCTAGAAACAGCCAATTAC
 ATTGACTTGAAGTGGATTCTATAATTAAAAAATTCTGGGCATGGGATAATGTT
 AGGTATTGCTAAGTCAGGCAGCCCTATCCCTCAGCAGAAGTGGAGGAATATGAAAGTG
 TGTGAATGCTAACATAATTGGGAATATGCCGTAGATTCCAGATGATATTCAAC

 20204 TCTGCCAGTTGCGAAGACTGGGAAAGCACAGTATTGGCAGAGTATACTGTTCTCCA
 GGTACAGTCACTCACCCCTTCTGGTAGGAAAGGGAAATCCCTGACCCCTTGCAC
 TCCTGGATGAGGTGACGTCCTGCCCTGTTGGCTACCCCTCATGGCTGACCCACTG
 TCCAACCACTGCAATGAGATGAAACAGGTACCTCAGTTGGAAATGAGAAATCACCC
 CTTCTGCATCGATTTGCTGGAGCTGTAGACCAGAGCTGTTCTACTGGGCATTTGG
 [G, A]
 AGCAACTCTGGTCTGAGTTCTGTTGTCCTGATGTATATCCCACTGCTAGAAT
 GATACTTGTACATAGGAAGTGCTTGTACATGTTGACAAATGAATCTTCTCATAAT
 GAGGTTCTCTAAACAAGCTGTTCTCCAAAACCTACACCCAGCTTATGTTGAAGCAT
 CTCATTATACATTGGAAAGATGAAATGTGAGACTTGAATCTCTTTGAATCTA
 GAAACATTAGCATTTAGACCATTCTATTAAATATTATGAAATTATGAAATAATAA

 20362 CCTCCATGGGCTGCACCCACTGTCACCGAGTGCAATGAGATGAAACAGGTACCTCAGT
 TGGAAATGCCAGAAATCACCCATCTCTGCATCGATTTGCTGGAGCTGTAGACCAGAGC
 TGTTCTACTGGGCATCTGGAGCAACTCTGGGCTGAGTTCTGTTGTCATGGCCTGA
 TGTATATCCCACTGCTAGAATGATACTTGTACATAGGAAGTGTGCTGATCCATGTTG
 CACAAATGAATCTTCTCATATGAGGTTCTCTAAACAAGCTGTTCTCCAAAACCTTA
 [C, A]
 ACCCAGCTTATGTTGAAGCATCTCATTATACATTGGAAAGATGAAATGTGAGAC
 TTGAAATCTCTTTGAATCTAGAAACATTAGCATTAGCATTGACCTTCTATTAAATATT
 TATGAAATTATGAAATAATAAGAAACATGAGGCCGGCTCAGTGGCTTATGCTGTAAT
 CCCAGCTTGGAGGCCAGGGCTAGTGGATCATGAGGTCAAGGAATTGAGACCAGCTT
 GGCAACATGGTAAACCCACTCTACTAAAAATATAAAATTAGCTGGCGTGGTGG

 21166 TAATTCCGCCATTGTTGCCTTGATCTTGGGCCATGTCATGTCATATTGATT
 TCTGTGTTTACGGTTCCATTCTCAGATCTCCCTGAGTTAGAAATCTGGCTGAGAAA
 TACCAAACAGTGATTGCCGACATTGCCGGAGAATGGCATTGGGATGGCAGAGTTTG
 GATAAGCATGTGACCTCTGAACAGGGAGTGGGACAAGGTTAGTCTCATAAAACAGTGTCTG
 TGTGTGATGTATTAGACAGAGCTGGCAGTCCTCATAGTGAAGCTCAGAACAGAAAAGTT
 [G, A]
 TCCAGTATTTTACGCCCTCTGGTTTACAATTCTGTTAGGTTGAATGTCATCA
 TAACAGTTATTCCAGAGTTAACCTCAACCCAGCAGCTATGAGGATATGCCAGGCT
 AGGAGTAGGGTACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAG
 ATTAACACTACACATCAAACATAAGGTAGGGTTAGGAGTCTTGCCTATTTCATAGGA
 ATGGTGGTTGTGAGACTTACTCATCACTTGTGAAAGACATTATTATTT

 21477 TCAGCCCTCTGGTTACAATTCTGTTAGGTTGAATGTCATCATAAACAGTT

FIGURE 2S

ATTCCAGAGTTAATTCAAACCAGCAGCTATGAGGATATCAGCCAGGCTAGGAGTAGGG
 TACTGGAGAGAAGTGCTTATCTAGACAAAGGGATGTAATTGACCATGAAGATTAAAAC
 CACATCAAACATAAGGTAGGGTTAGGAGTCTTGCCTATTTTCTAGGAATGGTGGTTG
 TGAGACTTACTCATCACTCTGTGGAAGTAAGACATTTATTATTAAAGCCA
 [G, A]
 TCAGATTAGCAGGCAGAGACATTCAAGACATCTAAAGTGGATGTATTCATACCTTT
 AACTGTGCTTAAATTAGGATCTCGAAAAGATGCTGCTACATGGTCACTACGTTAGTGT
 GGTCCAAGGGTCTTGGGCTCTTAAATTAAACCTCAAAACTTGACAGCAGTTATCTTT
 GGAACCTGCTGATTGTGCTTCTAAGTTAACAGCATACAATGACTGCTAGAAATCAATT
 CTGCATTAAAGGTGAAGTTAGCCGGTACTATGGTTACCTGTAATCTCAGCACTTGGG

 22230 GGATTGCTTGAAGCCAAAGAGTTGAAGGGTTGAGCCATGATTGTCCTACTGCACTCC
 AACGTGGGTGACAGAGCAAGACACCTACTGAAAGAAAATAAAGTTGAAGTTAAAACCT
 GGCAAGAACCAACGCACTGGTATGATAGTAACTCATTTCCTGTCAGATTAACTCAG
 GAAAATTAATTAAAGGTGTTGAATAGAAGTTTGATCAGATAAAATTGAATTAAAAAA
 ATTTTTTGAGACAGGGTCTTGTGTTATCCAGGCTGGTGTAGTGGTGTGATCACGG
 [C, T]
 TCCCCCGCAGCCTCAACCTCTGGCTCAGGTGATCCTCCACCTCAGCCTACCGAGTAGC
 TGTAACACAGTCATGACACCATACCAGGCTCATTGGTACATTGGTAGAGAGAG
 GGTGGCCATGTTGCCAGGCTAGTCTCAAACCTCCGGCATCAAACAGTCCTCCACTC
 TGGCCTCTCAAATGTTGGGATTACAGGCATGACCAGCCAATTATTCAGGAGTTATT
 TTTCTCTACTTTGGGAGATGAATTATAAGTCCTCATTAGGAGTATTCTAC

 22941 AATTCTGTCTACCTAATTCAAGGTTCACTCTTCTATGTTACTTTGTCCCAGA
 ACAAAATTCAAGTGCTTCTCTCACCTGTGCAATTCTCCCCCTGATTAGTCCTGGCTT
 TGTTACTTTCAAGTCAGAGACGACTTTTTTTGAGACAGGGCTCAGTCACCTGTCACC
 CAGACTGGAATGCGAGGGCACAGACAAGGCAGCCTTGACCTCTGGGCTCAAGCAATCTT
 CCTTGCCCTCAGCCTCTGAGTAACGGGACACAGGCACGTTGCCACCATGCCCTGGCTA
 [A, G]
 TTTATTTAATTAAAGGTGAGACAGGGTATTGCTCTGTACCCAGGCTGGAGTG
 TAGTGGCATGATCAAGGCTACTGCAGCCTTACCTCCTGCTCAAGCAGTCCTCTCAC
 CTCAGCCTCCCCATTAGCTGGACTATAGGTCACACCACACCCAGGCTAATTGGT
 AATTGGTAGAGACAGGGTTCATGTTGCTAGGCTGGTCTGAGCTCCTGGC
 TCAAGCGATTCACCTGCCATTAGCCTCCAGGTGTGAGCCACTACACTCAGCCTTTAAAA

 23963 ATACTACCTAGTTGAACCTTACCTAGCCCTGCCACAGACACGGCAGCCCTTGAAACCTTC
 CTGGGTTCAAGCGAGCCTCTACTTCAGCCCCCTGAGTAACGGGACACTGGCCTGTGT
 CACTGTGCTGGCTAATTCTTCTCCTACATGGGCAATGGTGGCAAGTTAAATC
 GACTCTTGTGCCCTAGTTCTCATCTGAATGGAGATCATACTGCTATGTACCTGAT
 ACAATGTTGTGAGGATTGAATGTCAGAGTTCTTCTGTTGTTGAGCTGGTGGAGA
 [C, T]
 GGAGTCTCACTCTG

 25686 CTGAAAATCTTAACTCTTGTGGTGCAGGAGACAGAAAACAAGCCAGGCCTCCCC
 AGGCAGCATAAGGGGATGGAAAATAGGATAGATTGACATGAGTTGCTTCAGGTAGAC
 TGGCTGACTCCCAGGATTACACCCACGTAATCAGTATATTCAAGCCTGCTGCTCTGAT
 TTCTTCTGAGCGGTCTTCTCAAGTGGTGGATATGGTACAACCCACGTGCACTAGCTT
 AACAAAAAGTTCTAGGAATGGCTTGTGCCCTGGCGAGTGGCTCATGCCCTGAATC
 [A, C]
 CAACAGTTGAGAGGCCAAGGTGGCGGATCACCTGAGGCCAGGAGTCAGAGACCCGCT
 GGCAACACATAGTGAACCCCGTGTAACTAAAAAATACAAAAATTAGCCGGCGTGGTGG
 CAAGGGCTGTAATCCCAGCTACCTGGGAGGCTGAGGCGAGGAGAATCGCTGAACCCAGG
 AAGCAGAGATTGCGGTGAGCTCAGATTGTGCCACTGCACCTCCAGCCTGGCGACAGAGTG
 AGACTCCCTCTAAAGAAGAGGAAGGGCTTGGTTCTGCTCAGCCTGAATCAGTTA

 26018 ACCTGAGGCCAGGAGTCAGACAGCCTGCCAACATAGTGAACCCCGTGTAACTAA
 AAAATACAAAATTAGCCGGCGTGGTGGCAAGGGCTGTAATCCCAGCTACCTGGGAGG
 CTGAGGCGAGGAGATCGCTTGAACCCAGGAAGCAGAGATTGCGGTGAGCTCAGATTGTGC
 CACTGCACCTCCAGCCTGGCGACAGAGTGAAGACTCCCTCTCAAAAGAAGAGGAAGGGCTT
 GGTTCTCTGCTCAGCCTGAATCAGTTACTGCTACACAGCTGAGTTCTCTGCCCTC
 [A, G]
 CCTGGATTACGTCTACACAGTACACACAGAATGGATTCCCCAAAGAAAGAATTCTGCG

FIGURE 2T

GCAGGAAGGGAAAGGGATGGCAGGTAGACAAAAACTCCAGGTGTCTGTAATAAGGGACA
 GGGTCGATCTTAATTAAACATGGACAGGGAACAGAAAGCTTTGATACTGATTGTT
 CAGAAGGAAAGTAGAAATTATGACTGTTCCCTGAATTATTCCAGCATTACCTTT
 GCTTCCATAAAAGTGTTCCTGCAGCCAAGTACTTTAAAGTTAAAAGACGGGTGAG

26078 AAAATACAAAAATTAGCCGGCGTGGTGGCAAGGGTTGTAATCCAGCTACCTGGGAGG
 CTGAGGCAGGAGAACGCTTGAACCCAGGAAGCAGAATTGCGGTGAGCTCAGATTGTC
 CACTGCACTCCAGCCTGGCGACAGAGTGAAGACTCCCTCTCAAAGAAGAGGAAGGGCTT
 GGTCTTCGCTCAGCCCTGAATCAGTTACTGTGACTACACAGCTGAGTCTCTGGCCTC
 ACCTGGATTACGTCTACACAGTACACACAGAATGGATTCCCCCAAAGAAAGAATTCTGC
 [G, A]
 GCAGGAAGGGAAAGGGATGGCAGGTAGACAAAAACTCCAGGTGTCTGTAATAAGGGACA
 GGGTCGATCTTAATTAAACATGGACAGGGAACAGAAAGCTTTGATACTGATTGTT
 CAGAAGGAAAGTAGAAATTATGACTGTTCCCTGAATTATTCCAGCATTACCTTT
 GCTTCCATAAAAGTGTTCCTGCAGCCAAGTACTTTAAAGTTAAAAGACGGGTGAG
 GCTAAGTGTGGTGTCTACACTTATAATCCAGTGTGAGGCCAGGAGTTCAAGACCAGC

26625 TGTGGTGTCTCATACTTATAATCCAGTGTGAGGCCAGGAGTTCAAGACCAGCCTGAGC
 AACACAGCAAGATACCATCTCTATAAAAATTGTTAGAAATGATTCTGCTAAAGAGCA
 AAAATAAAATTAAAGAAAGTAGAAAAAATAAAACAAATTAAAGATTAACTGGCAT
 GTTGGCATGCACCTGATTCTCTAGGTATTGGGAGGCTAAGGCACAAGGATCCCTTGAGC
 GCAGGAGCTCAAGGTTGGATTGAGTTGTAATCACACCAGTCAGCCTCCAGCCTGGTGGCA
 [C, G]
 AATGAAACTGTCTCAAGAAAAAAAGTGACAGAGGGAAACAATATTGCAATTCTATA
 GAGCAGATACAGGGTTCATATTCTTAATATTAAAAAAACTCTAAAAGTTAAAGAAAAAG
 GCCAACTGCCAACAGAAAATGGCAAGGAGATAAGAACAAAGATTGTCACAGGAAGAG
 ACACACAGATGATTATTAAAATCTGAAAAGATGCTGAGTCTACTCTAAAGAAAATTCT
 ACATTAAACTACTCTGGGGCTGGCAAGGTGGCTCACGCCGTAACTCAACACTGGG

27151 TCCTAAGAAAAATTACATTTAACTACTCTGGGGCTGGCAAGGTGGCTCACGCCGT
 AATCTCAACACTGGGAGCCAAGCAGGAAGATCACTGAAGCCAGGGATCGAGACCAGC
 CTGGACAACTGAGCTTATCTCTTAAACAAAACAAAACAAAACAAAA
 AACAGTAAAAATTGGCCGGCACAGTGAACCTCTGCCTATAATCCCAGCACTTGGGAAGC
 CCAGGTGAGTGGATCAACTTGAGGTCAAGGTGTTGAGAACAGCCTGGCAACATGGCAAAA
 [C, T]
 TCCGTCTCTACTAAATTACAAAAATTAGCCAAGTGTGGCATACTGGTAGGGCCA
 GCTACTTGGGAGGCTGATGTGAGACTCCATTAAAAAAATCAAATTAGCTGGG
 TATAGTGGCACACCCCTATAGTTCTCGCTCTGGGAGGGTGGAGGAGGATTGCCTG
 AGCCCAGGAGTTCAAGGCTGCAGTGAACCATGATCACACCAACTGCATCTAGCAGCCTGG
 GAGACAGAGCAAACCCCTGTCTAAAACAACAAACAACAAAACAAAAACACTT

28032 AGGAGCAGAGCCCTGCTTTCTCATTCACTTACTTTATCTGTAATAGCATCTTCTA
 CCACACGGTGGTGTGAATAAAATGAGATGAACCTCTAGCATAGAGTGCTTAGAAAG
 GTTCTGGACATTCGCTAGTTGAATCATGCCAAATGTGGCTCTAGGTGATTGGCTCT
 TTTGCTAGCATGTTTCAGGGCTCTCCATGCTGGGCATTGCACTACTGCTTTATTCT
 TTTTATGCCCTAGTATTATTCCACTGTGTGGATAGACCACATTATCATTCACTGTT
 [G, A]
 AGGATATTGGGTTCTCCATTTTGGCTATGGTAATAGTACTGTGTACATTG
 ATATAAGGTTTGTGAGATGTGTTTCTTTCTGGGCTATGCTGAGAAGTGG
 ATTGCTGGTTCATACAGCAGCTCGAACCTTGTGAGGAGCTGCCAGACGCTTTCCAAGGT
 CGCTCCACCACTTACATTCCGTCAGCAGTGTGAGAGTCCCAGTTCAACCAGCACTGT
 TGTTATCTTTTAACTGTATGTATATAACTTAACATTATTATAATAATGTACA

28772 AAAATCATCAAGCCGAATCCCACTGTTAGAATTAAAGGTTTATTCACTTCAAGTTA
 TCAGGATCCAGGGAGGTGAATACACTTAGAGGATAGACTCAGCTCATTCCCAGCTATG
 CCTTCAGCAGCATTCTTACCAAGAGTAGGAATATAATGTTAGTCATTATTAGAGGCTG
 GCCATCTTGAGAACGGTTACTGTTAGTCAGTACAATTATAACTGTTTGTATATT
 GGTTATTGGGCTAGAAGTAGGCCAGTAGCTCTAACAGGAGCCTTTAGCCTGAATT
 [G, A]
 TCCAAGTAGTGCAGTGTGCACTAGTTGTCCCTGGGACATGCTCCCAATACGTAAC
 ACTTCCAGGGTGCACACTGGACACTTACTGGTAGTCAGAAATAGCTATTGCA
 AAATGAACATTGATCTCGTAAAGATGAGTCTGCAGCTAACAGAGACTTACTGTATATCAT

FIGURE 2U

29572	<p>TCATAGTTCTTATGCACAAAGACCTTAATATTGTTGTAATTCTCCCTATGCACAC GCTGACCTGTTCTTAATCTTCTTATCTGCTAGGTTGGAGCAGGTATGTTAAGAAGTT AGGGGATTTGCTAACGCCGAGAATATTGACTTGGCCGTGCAGTCCTGAATGAACCTTAT AACCAATGCACTGCACCACATCCAGATGTCATCACCTACCTTCGAGACTCAGAAACCA GAGTGTGTTAACCTCTGTCTATTCCACAGGTAGGGAACGGGCTCCTCTGGGTGGATA [C, T] GGGGCTAAAGGGAGTGGGTAGGAGTAAGGGGGATTTGCTGTGCTATATTCAAGGATA TGATTCCCTTAAAAGACGATGACTCCAGTTATTACGCTGGGAGTTCATAGCACCGCC TTGCTTCCAGCACCACAAACTCAGCTCAGCCTTGAGGTTAACGCTGCTCTTCAAGAAC CTTCTTCCGGATTTACTATTCTACAGCTATCCTAAACTAGTTAGGTTCTTCTCA CAGTTAACGTCAAGGTCTTGGCTTAGATTATGGGGAGTGTGGTAAACCTGGGTGAA [C, T]</p>
29761	<p>ACTGCACCACATCCCAGATGTCATCACCTACCTTCGAGACTCAGAAACCAAGAGTGTGTT TAACCTCTGTGCTATTCCACAGGTAGGGAACGGGCTCCTCTGGGTGGATAACGGGCTAA AGGGAGTGGGTAGGAGTAAGGGGGATTTGCTGTGCTATATTCAAGGATATGATTCTC AAAAAAAGACGATGACTCCAGTTATTACGCTGGGAGTTCATAGCACCCGCCTTGCTC CAGCCACCAAAACTCAGCTCAGCCTTGAGGTTAACGCTGCTCCTTCAAGAACCTTCTTC [C, T] GGATTACTATTTCTACAGCTATCCTAAACTAGTTAGGTTCTTCTCACAGTTAACG CAAGGTCTTGGCTTAGATTATGGGGAGTGTGGTAAACCTGGGTGAAGCTGTTATC ATAAAAAAAGCTTCATTAAGCACCTAATTACTGCTGTCTTCTAGACCCGCTAA AAGAACCTGGTCCGGTAGACCTAGCCTCTCAGTATGCTAGGAACCTACACTTTAGTTG CCTTACCAAGTATTGCAAGATACTACTGCAAATAAGTGAAGAAAGTAACAGCATTAACT</p>
30732	<p>ATTCTGTGTGTTGAGAAAGGGAGGAGTGGGAAGGTTAAAAATCTTGACATACTTTCT TCGTGGTATTTTCTTGAGCGATTCCATCTTAGTTGATTGAGCTAGTTAGCAATTGCCA TTCAACAGAAGGTTTCTTACCTTTGTGATAATGATAGCTAACGACATCATTCTCT TTTTCCCTCTCTTCTTAGGTGATGCCATTGCCACTTGGCTGCTGTTA TAATAACCAGCAGGTGTTCAAAGGGCAGTGAAGATTGGAAAGGGCAAGCAGTGACCCCT [G, C] ATGATGGATGCCACCAATATGCCAGCTGCAAAGCCATCATATATCAGTATATGGAAGAG GTGGGTTTATTTAACTACTTGGATAATTGTAGCTACTTTATGATTAGTAATGTC CTGTTAACCCAGGTTGGATATTAGATGATCCTAACAAATTCACTATCCTGTGCCCTAAAG AGACAGGAATTGATATCCTTATAAGGAAAAAAAGTCTATTACAGGAGCCGAGCAGATTG CTCACTGCTGTAGTACCTGGTAGAGGGAGATAATGGAGCAAGGCTGTAGGTTGGAG</p>
30841	<p>GCAATTGCCATTCAACAGAACGGTTTCTTACCTTTGTGATAATGATAGCTAACGACA TCATTCTCTTTTCCCTCTTCTTAGGTGATGCCATTGCCACTTTG GCTGCTGTATAATAACCAGCAGGTGTTCAAAGGGCAGTGAAGATTGGAAAGGGCAA GCAGTGACCTGTGATGGATGCCACCAATGCCAGCTGCAAAGCCATCATATATCAG TATATGGAAGAGGTGGTTTTATTAACTACTTGGATAATTGTAGCTACTTTATGAT [G, T] TAGTAATGTCACTGTTAACAGGTTGGATATTAGATGATCCTAACAAATTCACTATCCT GTGGCCTAAAGAGACAGGAATTGATATCCTTATAAGGAAAAAAAGTCTATTCAACAGGAGC CGAGCAGATTGTCACTGCTGTAGTACCCCTGGTAGAGGGAGATAATGGAGCAAGGCT GTAGGTTGGAGCCCTCAGTAGAAATCATAGATTGTAGCTGCAAGATGATGCAAGGAGG AACCAAGCTTCTTGTGCTGGTAGGAAATGTGAGGTTGAAGCTTGTGCTGATGCG [G, A] TTCAAAAAGTTTATTCTGGCCAGGCACAGTAGCTTACTCCTGAAATCCCAGCACTTGG ATGCACTGCGTGTGATTGAGTGGATCTCTGGCTCCCATGTCCTGACACCCAGTCTG GTACTTTATTAGCCACAGGCCCAATTGAAAAATCACAGTAGGAAATTAGGCAAGG AAAGCCATCAAGTGCATTATTTCTAAATTTCCTTGGAAAATTCAATTCAAATAC AAAACCATCCTATAAAAAGAAAATTACCTTCTAGGTCAAATCTTAATTGACTAG [G, A] TTCAAAAAGTTTATTCTGGCCAGGCACAGTAGCTTACTCCTGAAATCCCAGCACTTGG GAGACCAAGGTGGAGGATCACTTGAGGCCAGGAATTCAAGACAGGCCGGCGACATAG CAAGACCCCAATTCTACAAAAAAATTAAAATTGTGATGGTGGTGCAGCCTGTTGGTCC AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTCAGGCTACAGT AGCTGTGTGATTTCATCATTGCACTCTAGCCTGGGTGATAGAGTGAAGACTTTGCTCAA</p>
31376	<p>GAGGCCAACCAAGCTTCTTGTGCTGGTAGGAAATGTGAGGTTGAAGCTTGTGCTGCTG ATGCACTGCGTGTGATTGAGTGGATCTCTGGCTCCCATGTCCTGACACCCAGTCTG GTACTTTATTAGCCACAGGCCCAATTGAAAAATCACAGTAGGAAATTAGGCAAGG AAAGCCATCAAGTGCATTATTTCTAAATTTCCTTGGAAAATTCAATTCAAATAC AAAACCATCCTATAAAAAGAAAATTACCTTCTAGGTCAAATCTTAATTGACTAG [G, A] TTCAAAAAGTTTATTCTGGCCAGGCACAGTAGCTTACTCCTGAAATCCCAGCACTTGG GAGACCAAGGTGGAGGATCACTTGAGGCCAGGAATTCAAGACAGGCCGGCGACATAG CAAGACCCCAATTCTACAAAAAAATTAAAATTGTGATGGTGGTGCAGCCTGTTGGTCC AGCTACTCAGGAGGCTGAGGCAGGTGGATCACATGAGCCTGAGAGGTCAGGCTACAGT AGCTGTGTGATTTCATCATTGCACTCTAGCCTGGGTGATAGAGTGAAGACTTTGCTCAA</p>

FIGURE 2V

32032 TCTCTAGGCCCTAGAGCAGTGGTTGAAATGGAGGTGATTGCTCCCTCCCCCAGAG
 GACATTGGACAATGTCGGAGACATTTGATTGCTCTAACCGGCAGGAATCGGGTGCTA
 CTGGCATCTGGTAGAGGAGGCCAGGATGATGCTGATCCTCAGGTGTGATCCTGTTG
 AGAATGAAACACTGTAGACTTATGAAAACATACAAGACCTCATCTTCTTCTTGC
 TGAGCTCCCTCCCCAGAGGTACCTCTGTTCATGGTTGTCATCGCTAGTCCCCCT
 [A, G]
 TTACCGCGTTACAGGAATATGGTTGCAACAGTGTTCATCTAAATAGAATTATACAAA
 ATAGCGATTCTGATTCTCTGCATATTGCACATTCTCTTAACTCTCCCTACCTT
 TATCTGACACAGAAATGCTGTATGTCAGAACTCTATCAGAGGCACCTATGAAAGTCTA
 AGGGAAAGACCACATCGCTTTAAAAACCTAAAATTGTTAGTCACTAGATGAAAATATT
 CAGCCAGTACCCAAAAATTGCTACCAATGAGACTCTCCATTGCCATGTAGCCAGAA

 32525 ATCGCTTTAAAAACCTAAAATTGTTAGTCACTAGATGAAAATATTCAAGCCAGTGACC
 CAAAAAAATTGCTACCAATGAGACTCTCCATTGCCATGTAGCCAGAACTTACTTGATC
 TATGTGCTCGGGTAGTGACCAAGTAGGTGGTAGGAGTAATCTCAGGGAAACTTGAGGC
 CCCAGCCTCATGGCTAGGGTCTAAATTGAAACCCAGGTCTGTCGACATCAGAATCCATG
 ATGTTAACCCAAATTCTAACGGGTTCAACTACCCCTTCTAAATGAACTCTGCTATATTA
 [A, G]
 GCACTATTATTCACTTATATAAACTAGAAACATTTATGTTAGTAAGTAGTTGAGAGTG
 TTTGGTTTGCAAGTTGATCACTAGTTAGAAACAGTTTAAACACTTGTGGCCA
 ATTCCATTACTATATTAAATTCAAGATTATTGGTTTCCTTAACATTTGGGATTA
 TCCCTGGTTGAAATTCAAGTTGAGGGCGAGGGTGGGAGTCTACATTGCTGAGCCCT
 GTTTGTGAATAATGTTATCAGAACACAGCCACACCCATTGCTCTATGCTCTGT

 34179 CTGCTGTATGTTAGCACAGCATTGCAAGAGCTTATTCAGTCTAGTAAACATTATAGG
 AGCCTGTGTCATTTAATCATCAAGCCTCGCACTGTCAGCTCACACCTGTAATCCAAA
 TTGGGAGGCTGAGGCAGGCGAGATCACTTGAGGTAAGGAGTTGAGACCCAGCCTGGCCA
 ATGGCAAAACCCCTGTCCTACTAAAATACAACATTAGCCAGGTGTTGGTGGTGCACACT
 TGTCACTCCAGCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACCTGGGAGGTGGAG
 [G, T]
 TTGTAGTGGAGCTGAGATGGCACCCTGCACCTCCAGCCTGGCAACAGGGTGAAGGCCCTT
 TCTCAAACCTCTCAAGTATTGGCTCAACTTATGCCGGCATGTAGATGAAAAGTCGG
 CTATGACCTGTCCTTGACAAGCAGATGTAACCTTGATTGAGGCTAGTAGGTTTTAAG
 ACCTGAATAATTGAGTTGCAAGAACCTACTGTGTGCCTTCAGGTAATGGAGAGTGGG
 TTGGTCTAGCAACGAAGCATCTAGAAGGTCTTTGGCCTTACCGGCTCTGGT

 34249 ATTTAATCATCAAGCCTCGCACTGTCAGCTCACCTGTAATCCAAA
 GAGGCAGGCAGATCACTTGAGGTAAGGAGTTGAGACCCAGCCTGGCAATATGGCAAA
 CCTGTCCTACTAAAATACAACATTAGCCAGGTGTTGGTGCACACTTGTCATCCCA
 GCTATTCCGGAGCCTGAGACATGAGCATCGCTTGAACCTGGGAGGTGGAGGTGAGTGA
 GCTGAGATGGCACCCTGCACTCCAGCCTGGCAACAGGGTGAAGGCCCTTCTCAA
 [T, C]
 CTCAAGTATTGGCTCAACTTATGCCGGCATGTAGATGAAAAGTCGGCTATGACCTG
 TCTTGACAAGCAGATGTAACCTTGATTGAGGCTAGTAGGTTTTAAGACCTGAATAA
 TTGAGTTGCAAGAACCTACTGTGTGCCTTCAGGTAATGGAGAGTGGGTTGGTCTAG
 CAACGAAGCATCTAGAAGGTCTTTGGCCTTACCGGCTCTGGTAAAGTCCACGT
 CTGAGTACCAAGTGAUTGCAGCTTCCAGTTGCTGTATGTTATATGTTAGAAATGA

 34451 GAGCATCGCTGAACTCGGGAGGTGGAGGTGAGTGAAGCTGAGATGGCACCCTGCACT
 CCAGCCTGGGCAACAGGGTGAAGGCCCTTCTCAAACCTCTCAAGTATTGGCTTC
 TTATGCCGGGATGTAGATGAAAAGTCGGCTATGACCTGTCCTGACAAGCAGATGTAAC
 TCCCTGATTGAGGCTAGTAGGTTTTAAGACCTGAATAATTGAGTTGAGAAACCTACT
 GTGTGCCTTCAGGTAATGGAGAGTGGGTTGGTCTAGCAACGAAGCATCTAGAAGGTC
 [T, C]
 CTTGGCCTTACCGGCTGTTTAGGTAAGTCCACGTCAGTACCAAGCTGAGCTGAGC
 CTTCCAGTTGCTGTATGTTATGTTAGAAATGATCATCAAAGGACTCAAAGTT
 TGCCACTAATTGTTACCGGGACTGTCACAACCAAGGATTTCTCTTAATTATTAC
 TACTTATCTCCTGGAAAGGGCATATTGAAGTGTCTTGGAGTTCTCTAAAAGGGTTTG
 TGTTGTGATATTCACTGGGTGCCAGCGATTCAAATAAGTAAATCTTTTCC

 34532 AGGCCCTTCTCAAACCTCTCAAGTATTGGCTCAACTTATGCCGGCATGTAGATGA

FIGURE 2W

AAAGTCGGCTATGACCTGTCCTTGACAAGCAGATGTAACCTCTGATTGAGGCTAGTAGG
 TTTTAAGACCTGAATAATTGAGTTGCAGAACCTACTGTGTCCTCAGGTAATGG
 GAGTGGGTTGGCTAGCAACGAAGCATCTAGAAGGCTCTTGGCTTACCGGCTCTG
 TTTTAGGTAAGTCCACGTCTGAGTACAGTGACTGCAGCTCTCAGTTGTGCTGTCATG
 [T, C]
 TTATATGTAGAAATGATCATCAAAGGACTCAAAGTTTGCCACTAATTGTATTACCGG
 GGACTGTCACAACCAAGATTTCTTAATTATTACCTACTTATCTCTGGAAAGGGCA
 TATTGAAGTGCTCTGGAGTTCTAAAAGGGTTTTGTGGTTGTATATTCACTTGG
 GTGCCAGCAGATTCAAATAAGTAAATCTTTTCCAAAAGGATGTAAGATGGCTT
 ATGGTTATAAGTACAACAGGCTAACAAAGTACAAGTAGATGAGAAGTAAAATGAAGAAA

36541 GGTAGGAGGCCAGTTGAAGGGACGTGGGAGGGCATTCCAGAGAGAAGGGTGGTATGAGA
 CTGGAACAGAGGTGTGCAGCAGCATCGCATGGCGAAACAAACAGTAGACAGTTGTTCTT
 TGTTTTGTTGTTTGAGACAGGGCTTGTCTGTCACTCCAGGCTCAAGTGTACCTCCCACCCAGT
 CATGATCTGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGTACCTCCCACCCAGT
 CCCCAGTAGCTGGGGACCACAGGTGCATGCCACGATGCCGGCTAATTTGTACATT
 [T, C]
 TGTAGAAACAGGGTTTACTGTGTTGTCAGGCTGGCTTAAACGCTGAGCTTAAGCAG
 TCTACATGCCCTAGCTCTGAAGTGTGGATTCCAAACATGAGCCACTGTGCCCTGGCC
 CGGCAACTGTTACTAGACTATAGAGAGGGAGGTGGCAAGGGCTGGTACACTAGACAGG
 TGCACTAGGTCTGGACCATGGGTGGCTTGCCTACACATTACAGAGCTCAGGTTTTT
 TCTCCAGGTGAGAGGGCTGGTGCCTAGAGGCATCAAGCAGAGGTTGAGATCTCTTGG

36607 CAGAGGTGTGCAGCAGCATCGATGGCGAAACAAACAGTAGACAGTTGTTCTTTGTTT
 TGTTGTTTTTGAGACAGGGCTTGTCTGTCACTCCAGGCTGGAGTGCAGTGGCATGAT
 CTCGGATCACTGCAACCTCCACCTCCAGGCTCAAGTGTACCTCCCACCCAGTCCCAA
 GTAGCTGGGGACCACAGGTGCATGCCACGATGCCGGCTAATTTGTACATTGTAG
 AAACAGGGTTTACTGTGTTGTCAGGCTGGCTTAAACGCTGAGCTTAAGCAGTCTAC
 [A, G]
 TGCCCTAGCCTCCTGAAGTGTGGATTCCAAACATGAGCCACTGTGCCCTGGCCGGCAA
 CTGTTACTAGACTATAGAGAGGGAGGTGGCAAGGGCTGGTACACTAGACAGGTGCAGT
 AGGTCTGGACCATGGGTGGCTTGCCTACACATTACAGAGCTCAGGTTTTCTCCA
 GGTGAGAGGGCTGGTGCCTAGAGGCATCAAGCAGAGGTTGAGATCTCTTGGTACAG
 TGTAGAGCAGACAGGTAGATTGGAATTAAAGCTTAGACTCACGTTGGAGACTGAGATA

36681 GACAGGGCTTGTCTGTCACTCAGGCTGGAGTGCAGTGGCATGATCTGGATCACTGCA
 ACCTCCACCTCCCAGGCTCAAGTGTACCTCCCACCCAGTCCCAAAGTAGCTGGGGACC
 ACAGGTGCATGCCACCATGCCGGCTAATTTGTACATTGTAGAAACAGGGTTTAC
 TGTGTTGTCAGGCTGGCTTAAACGCTGAGCTTAAGCAGTCTACATGCCCTAGCCTCC
 TGAAAGTGTGGATTCCAAACATGAGCCACTGTGCCCTGGCCGGCAACTGTTACTAGACT
 [A, G]
 TAGAGAGGGAGGTGGCAAGGGCTGGTACACTAGACAGGTGCAGTAGGTCTGGACATG
 GGTGGCCTTGCCTACACATTACAGAGCTCAGGTTTTCTCCAGGTGAGAGGGCTGG
 TGCCACTGAGGCATCAAGCAGAGTTGAGATCTCTTGGTACAGTGTAGAGCAGACAG
 GTAGATTGGAATTAAAGCTTAGACTCACGTTGGAGACTGAGATAGCTCATCTGAGAGG
 CACTCAGGGCTAATCTCAGGCAGTAATTTAGGGATGTAGGGAAAGAGATGGATTCTGC

37493 TGACGTTATTGGGCTGGCACTGTGAGGTGCTGGGATGTGAAGATCATTGTGGCTCAG
 CCGCTGCTCTCGAGGGCTCTGGGTGCAGTATGCACACCTGTGCCCTCTGTTGCTCAGG
 AAGACAGGCTTGGAGATGAGCTGGGCTGACATCCCACCTTATCATTGGATGGCTTG
 GGTAAGTTATGTTATGTTCTGTGAGCCTCCCTTCTCATTGGTAAATGGGTATAAAA
 TACCTGCCAGTGGAGGGTGTGTAAGTAGGCATGGAAAATGTAAGCAGCACATGCACTTA
 [C, T]
 CATTGTTCTGTGTTAACAGATTATCATAGAATCCCCGACTCAGACCCATCTTCT
 AGCAAAACAAGGCAGATCATCTCACCACCGACGCGAGAATCTCCAACTGTCACTG
 ATTTCCGAAGCCACTACTCCCCATCTACCTGTGTTGTACGCTTGGCTGCCCTG
 AGCTGGCAGTACCTGACCACTCTCTCCAGGTAAACAGAAGACTATGTTCAAGACTGGAGAA
 CACTGATCCAAATTGTCAGTGAAGTCCACCATAAGTGGATTACTTTTTCT

37966 CTGCCCTGAGCTGGCAGTACCTGACCACTCTCCAGGTAAACAGAAGACTATGTTCAGA
 CTGGAGAACACTGATCCAAATTGTCAGTGAAGTCCACCATAAGTGGATTACT
 TTTTTCTTAAGGATGGATGTTGTTCTTTATTTCCTACTACTTTAACCCCT

FIGURE 2X

AAAAGAACGCTGTGGCTGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAA
ACATGAAAGGAAAGGGCCTCATCCCAGCAACCTGCCTTGTGGGTATGATCACTGTG
[C, A]
TGCTTGTGGCTCATGGCAGAGCATTCACTGCCACGGTTAGGTGAAGTCGCTGCATATGT
GACTGTGATGAGATCCTACTTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAA
TTTGAAGCACCATTGAAATGTTCTGACTAGTAGAAAATGATGTGAATTTCCTGTT
GGCTCCTATTTCTCATCTTGTGTTCTTAATTGGGTTGAATGGAGTAGATAGAAA
TATTTATGGTTAGGTAACAGTTAGATGTTCTAAGAATGCAAACACTGCCTTCCACAC
37973 GAGCTGGCAGTACCTGACCACTCTCTCCCAGGTAACAGAACACTATGTTCAGACTGGAGA
ACACTGATCCAAATTGTCCATAGCTGAAGTCACCATAAAGTGGATTTACTTTTTC
TTAAGGATGGATGTTGTGTTCTTATTTCCTACTATTTAATCCCTAAAAGAA
CGCTGTGTGGCTGGGACCTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAA
AGGAAAGGGTGCCTCATCCCAGCAACCTGTCCTGTGGGTGATGATCACTGTGCTGTTG
[T, C]
GGCTCATGGCAGAGCATTCACTGCCACGGTTAGGTGAAGTCGCTGCATATGTGACTGTC
ATGAGATCCTACTTATGATCCTGGCTAGAATGATAATTAAAAGTATTTAATTGAAAG
CACCATTGAAATGTTCTGACTAGTAGAAAATGATGTGAATTTCCTGTTGCTCCT
ATTTTCTCATCTTGTGTTCTTAATTGGGTTGAATGGAGTAGATAGAAAATTTAT
GGTTAGGTAACAGTTAGATGTTCTAAGAATGCAAACACTGCCTTCCACACAAAGGCT
38113 TCTCTTATTTCTACTACTTTAATCCCTAAAGAACGCTGTGGCTGGGACCTT
TAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAAGGAAAGGGTGCCTCATCCC
AGCAACCTGTCCTGTGGGTGATGATCACTGTGCTGCTTGTGGCTCATGGCAGACATT
AGTGCACGGTTAGGTGAAGTCGCTGCATATGTGACTGTCATGAGATCCTACTTAGTAT
GATCCTGGCTAGAATGATAATTAAAAGTATTTAATTGAAAGCACCATTGAAATGTCGTA
[C, A]
TAGTAGAAAATGATGTGAATTTCCTTCTGTTGGCTCCTATTTCATCATTGTT
TTCTTAAATTGGGTGAATGGAGTAGATAGAAAATTTATGGTTAGGTAACAGTTAGAT
GTTTCTAAGAATGCAAACGCCTTCCACACAAAGGCTGGGAATAAAATTCTGGGTAT
TCTCGTATTCTCATTTAAAGGAGTTAGCTTCAGAGAGAACAGCAGGATTGCTTGA
CCTTTAGAAGATTGGCTCCAGTAAAGGTGGACATTGGAGATTATAATAAAAGAATT
38298 CACGGTTAGGTGAAGTCGCTGCATATGTGACTGTCATGAGATCCTACTTAGTATGATCC
TGGCTAGAATGATAATTAAAAGTATTTAATTGAAAGCACCATTGAAATGTTCTGACTAGT
AGAAAATGATGTGAATTTCCTTCTGTTGGCTCCTATTTCATCATTGTTCT
TTAATTGGGTGAATGGAGTAGATAGAAAATTTATGGTTAGGTAACAGTTAGATGTT
CCTAAGAATGCAAACGCCTTCCACACAAAGGCTGGGAATAAAATTCTGGGTATTCTC
[G, C]
TATTCTCATTTAAAGGAGTTAGCTTCAGAGAGAACAGCAGGATTGCTTGA
TAGAAGATTGGCTCCAGTAAAGGTGGACATTGGAGATTATAATAAAAGAATT
TTGCTCTGCATTGTCAAGTACAGTTCGCTTGAAGCCTGCCTGACTGTGGAAAAGATGG
AGCTCAAGAATGGAGTTGATGGCCAGCGTGGCTCATGCCTGTAATCCCAGCACTT
GGGAGGCTGAGGCCGGTCGGATCACGACATTAGGGGATCGAGACCATCCTGGCTAACACGG